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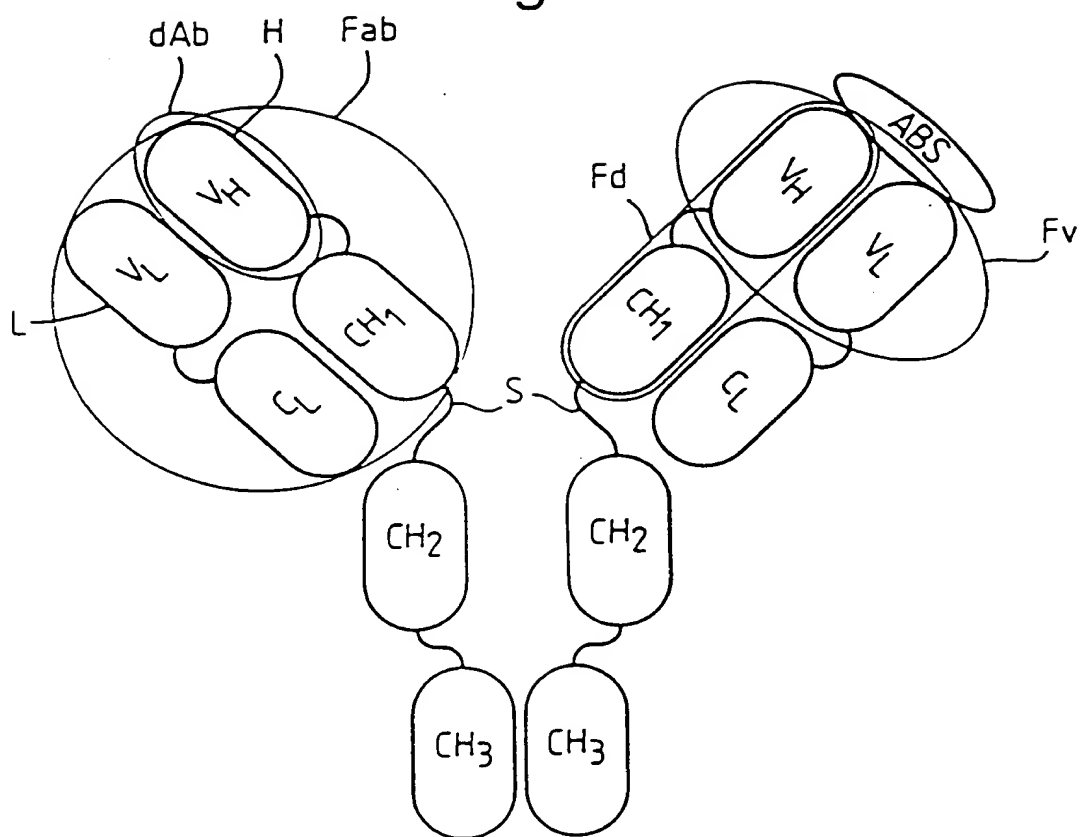
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Fig.1.



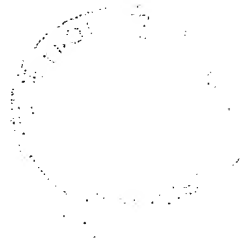


Fig.2 (i).

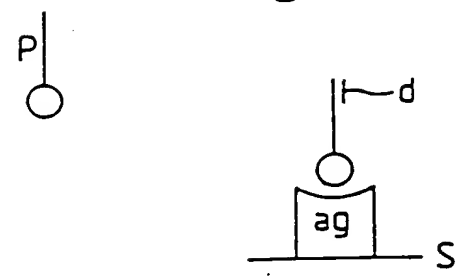


Fig.2 (ii).

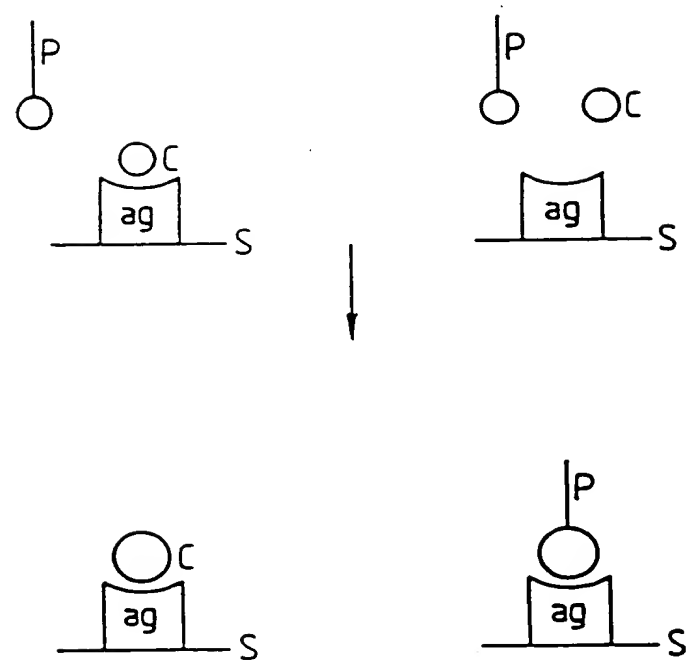
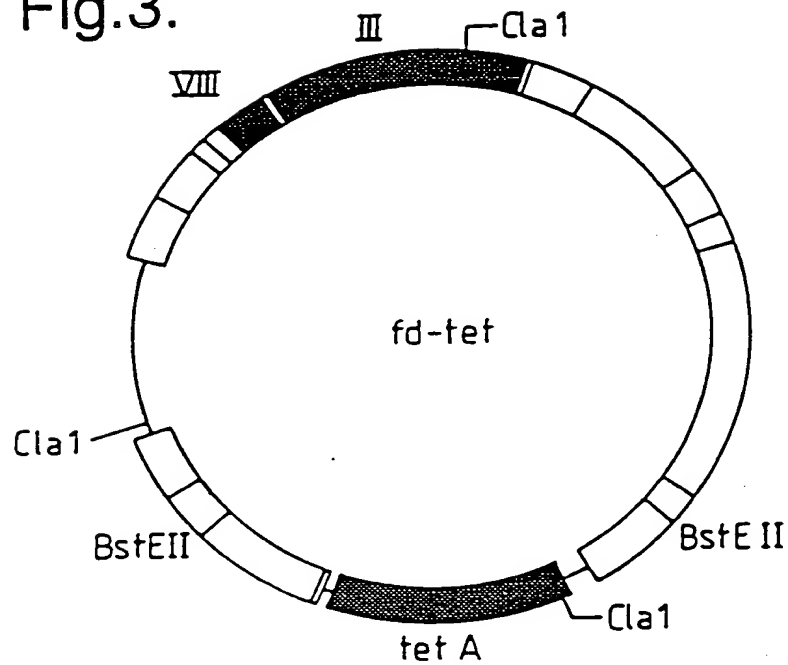


Fig.3.



fd - tet

~

cleave with BstEII

~

fill in with Klenow

~

re-ligate

↓

FDT6 Bst

~

in vitro mutagenesis (oligo 1)

↓

FDTPs/Bs

~

in vitro mutagenesis (oligo 2)

↓

FDTPs/Xh

(1653)
 Oligo 1 ACA ACT TTC AAC AGT TGA GGA GAC GGT GAC CGT AAG CTT CTG CAG TTG GAC CTG AGC (SEQ ID NO. 177)
 GGA GTG AGA ATA (1620)
 (1653)
 Oligo 2 ACA ACT TTC AAC AGT TTC CCG TTT GAT CTC GAG CTC CTG CAG TTG GAC CTG (SEQ ID NO. 178)
 (1704)
 Oligo 3 GTC GTC TTT CCA GAC GTT AGT (SEQ ID NO. 179)

Fig.4 (i).

GENE III

GENE III

SIGNAL
CLEAVAGE SITE

Fig.4 (ii).

(1624)
 A TCT CAC TCC GCT
 (1650)
 GAA ACTGTT GAA AGT (SEQ ID NO. 180)
 Q V Q L Q (SEQ ID NO. 1) V T V S S (SEQ ID NO. 2)
 B TCT CAC TCC GCT CAG GTC CAA CTG CAG AAG CTT ACG GTC ACC GTC TCC TCA ACT GTT GAA AGT (SEQ ID NO. 181)
 PstI BstEII
 Q V Q L Q (SEQ ID NO. 1) L E I K R (SEQ ID NO. 3)
 C TCT CAC TCC GCT CAG GTC CAA CTG CAG GAG CTC GAG ATC AAA CGG GAA ACT GTT GAA AGT (SEQ ID NO. 182)
 PstI XhoI

BstEII

Fig.5 (Cont).

E T V T I T C R A S G N I H N Y L A W Y
GAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTTCACAATTATTTAGCATGGTAT
550 560 570 580 590 600

Q Q K Q G K S P Q L L V Y Y T T T L A D
CAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATTATACACAACCTTAGCAGAT
610 620 630 640 650 660

VKD1.3

G V P S R F S G S G S G T Q Y S L K I N
GGTGTGCCATCAAGGTTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAAC
670 680 690 700 710 720

S L Q P E D F G S Y Y C Q H F W S T P R
AGCCTGCAACCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTGGAGTACTCCTCGG
730 740 750 760 770 780

Myc Tag (TAG1)

T F G G G T K L E I K R E O K L I S E E
ACGTTTCGGTGGAGGGACCAAGCTCGAGATCAAACGGGAACAAAACTCATCTCAGAAGAG
790 800 810 820 830 840

XhoI

D L N * * (SEQ ID NO. 183)
GATCTGAATTAATAATGATCAAACGGTAATAAGGATCCAGCTCGAATTC (SEQ ID NO. 184)
850 860 870 880

EcoRI

Fig.6.

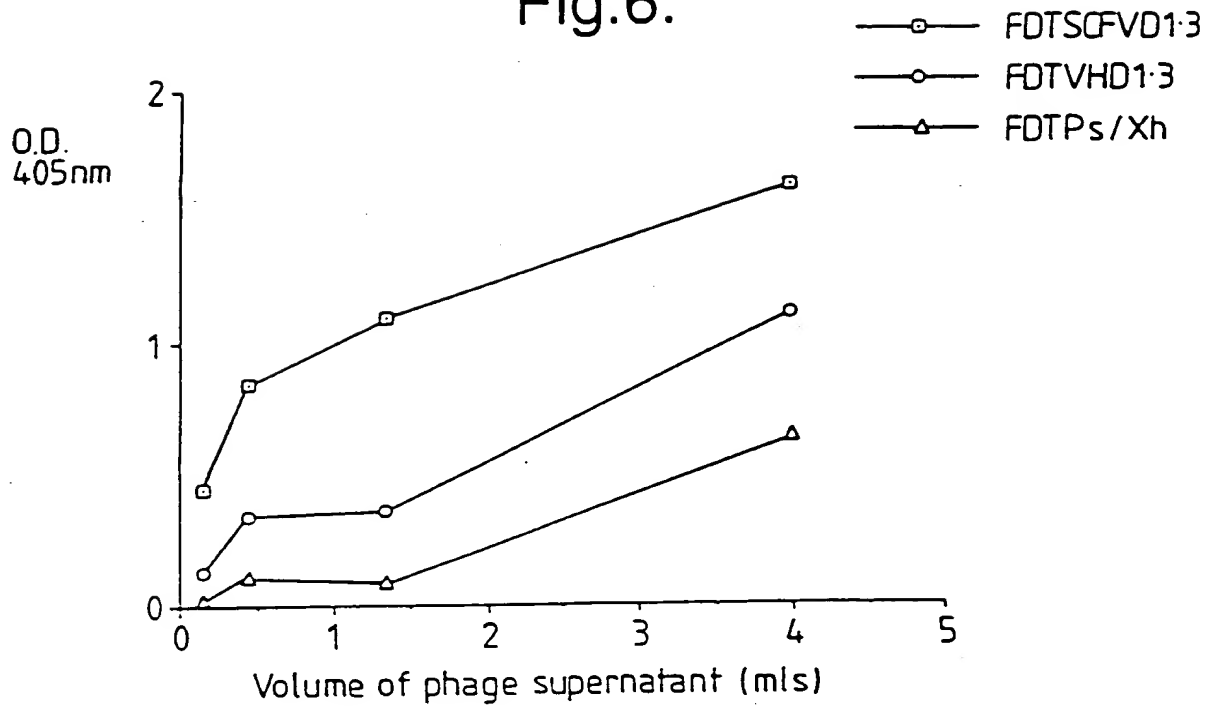


Fig.7.

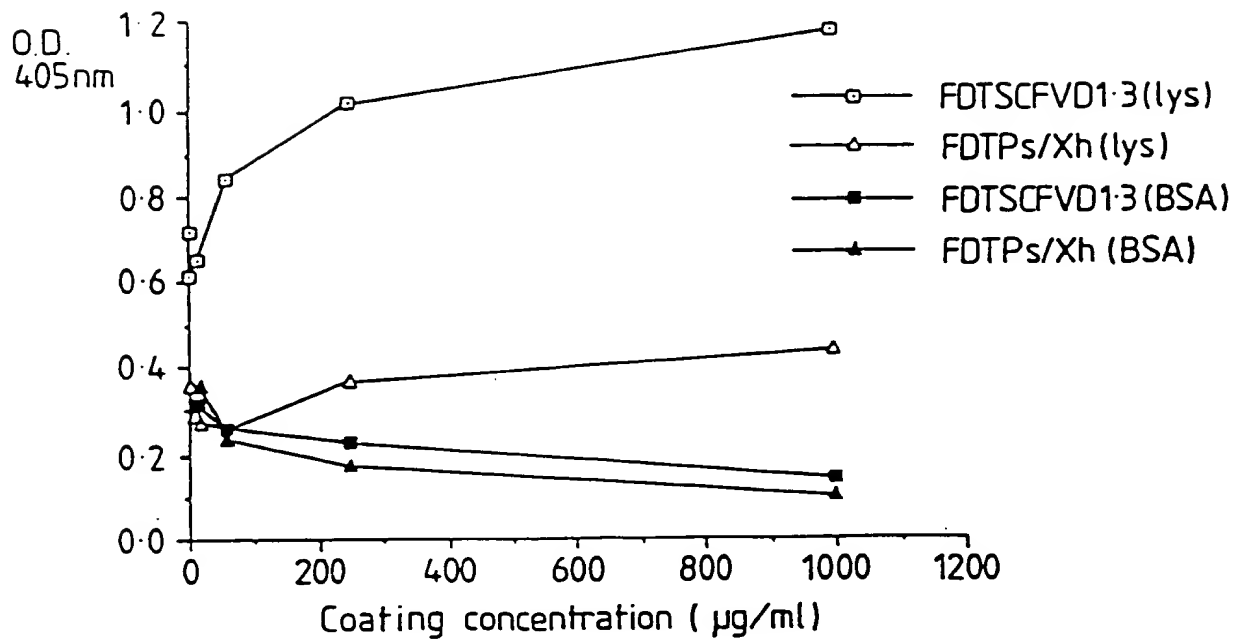


Fig.8.

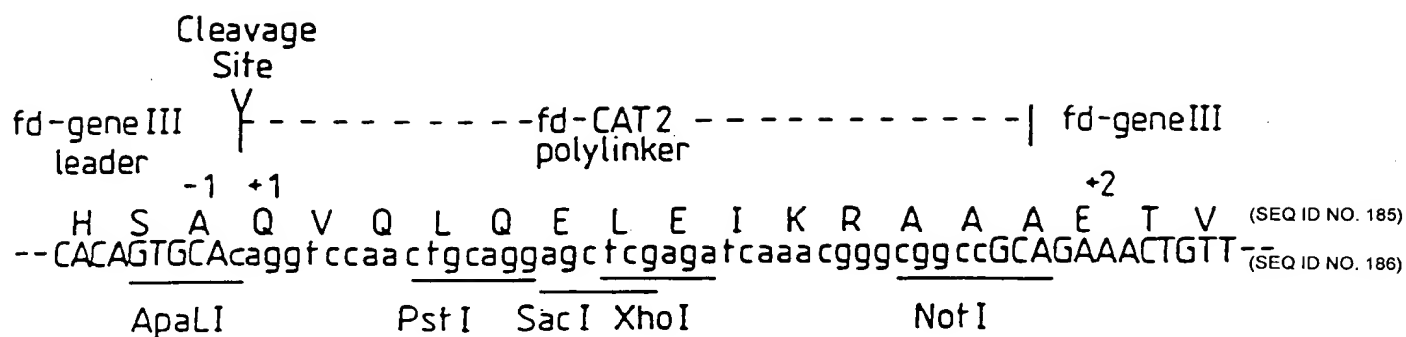


Fig.9.

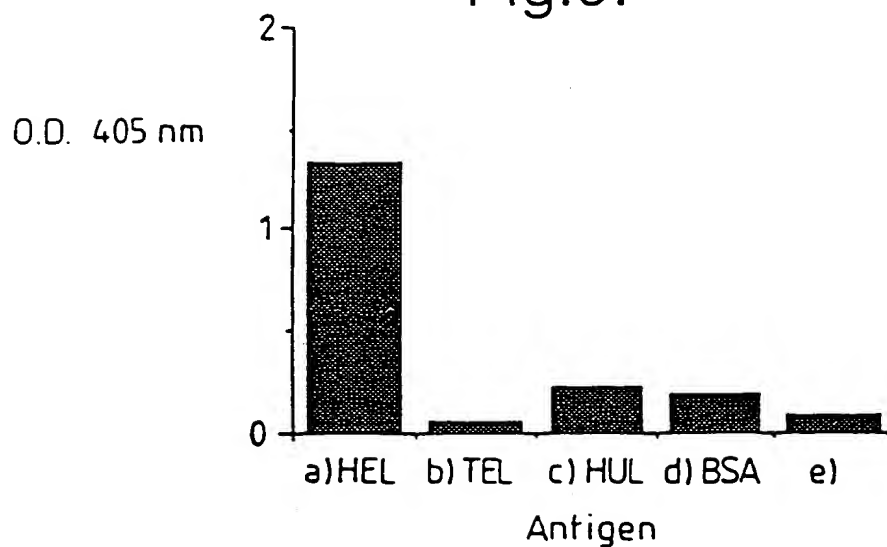


Fig.10.

M K Y L L P T A A
GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCGCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCCCAACCAGCGATGGCCCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAACTGGGTTCGCCAGCCTCCAGGAAGGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGOCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S A S T K G P S V F P L
CAAGGCACCAAGGTACCGTCTCTCTCAGCCTCCACCAAGGGCCCCATGGGTCTTCCCCCTG
430 440 450 460 470 480

A P S S K S T S G G T A A L G C L V K D
GCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGGCTGGTCAAGGAC
490 500 510 520 530 540

Fig.10 (Cont 1).

Y F P E P V T V S W N S G A L T S G V H
TACTTCCCCGAACCGGTGACGGTGTCTGTGGAACTCAGGCGCCCTGACCAGCGGGGTGCAC
550 560 570 580 590 600

T F P A V L Q S S G L Y S L S S V V T V
ACCTTCCCCGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGAACGTG
610 620 630 640 650 660

P S S S L G T Q T Y I C N V N H K P S N
CCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC
670 680 690 700 710 720

T K V D K K V E P K S S * * (SEQ ID NO. 187)
ACCAAGGTGACACAAGAGTTGAGCCCAATCTTTCATAATAACCCGGGAGCTTGCATGCA
730 740 750 760 770 780

M K Y L L P T A A A G L
AATTCTATTTCAGGAGACAGTTCATAATGAATACTTATGCTTACGGCAGCCGCTGGAT
790 800 810 820 830 840

L L L A A Q P A M A D I E L T Q S P A S
TGTTATTACTGCTGCCCCAACCCAGGATGGCCGACATCGAGCTCACCCAGTCTCCAGCCT
850 860 870 880 890 900

L S A S V G E T V T I T C R A S G N I H
CCCTTTCTGGTCTGTGTTGGAGAACTGTCAACATCACATGTCTGAGCAAGTGGGAATATTC
910 920 930 940 950 960

N Y L A W Y Q Q K Q G K S P Q L L V Y Y
ACAATTATTTAGCATGGTATCAGCAGAAACAGCGAAATCTCCTCAGCTCCTGGTCTATT
970 980 990 1000 1010 1020

Fig.10 (Cont 2).

T T T L A D G V P S R F S G S G S G T Q
ATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTTCAGTGGCAGTGGATCAGGAACAC
1030 1040 1050 1060 1070 1080

Y S L K I N S L Q P E D F G S Y Y C Q H
AATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAAC
1090 1100 1110 1120 1130 1140

F W S T P R T F G G G T K L E I K R T V
ATTTTGGAGTACTCTCTGGACGTTGGTGGAGGCCACCAAGCTCGAGATCAAACGGACTG
1150 1160 1170 1180 1190 1200

A A P S V F I F P P S D E Q L K S G T A
TGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTCTG
1210 1220 1230 1240 1250 1260

S V V C L L N N F Y P R E A K V Q W K V
CCTCTGTTGTGTGCTGCTGAATACTTCTATCCCAGAGAGGCCAAAGTACAGTGGGAAGG
1270 1280 1290 1300 1310 1320

D N A L Q S G N S Q E S V T E Q D S K D
TGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGG
1330 1340 1350 1360 1370 1380

S T Y S L S S T L T L S K A D Y E K H K
ACAGCACCTACAGCCTCAGCAGCA.CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACA
1390 1400 1410 1420 1430 1440

V Y A C E V T H Q G L S S P V T K S F N
AAGTCTACGCCCTGCGAAGTCAACCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA
1450 1460 1470 1480 1490 1500

R G E S * * (SEQ ID NO. 188)
ACCGCGGAGAGTCATAGTAAGAATTC (SEQ ID NO. 189)
1510 1520

Fig.10 (Cont 3).

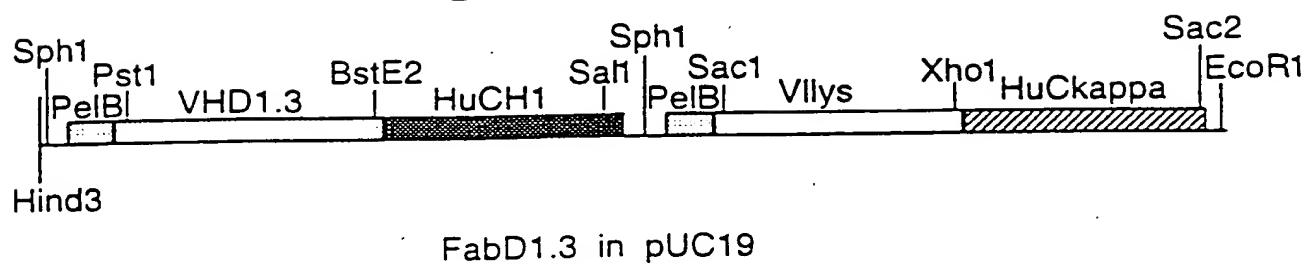


Fig.11.

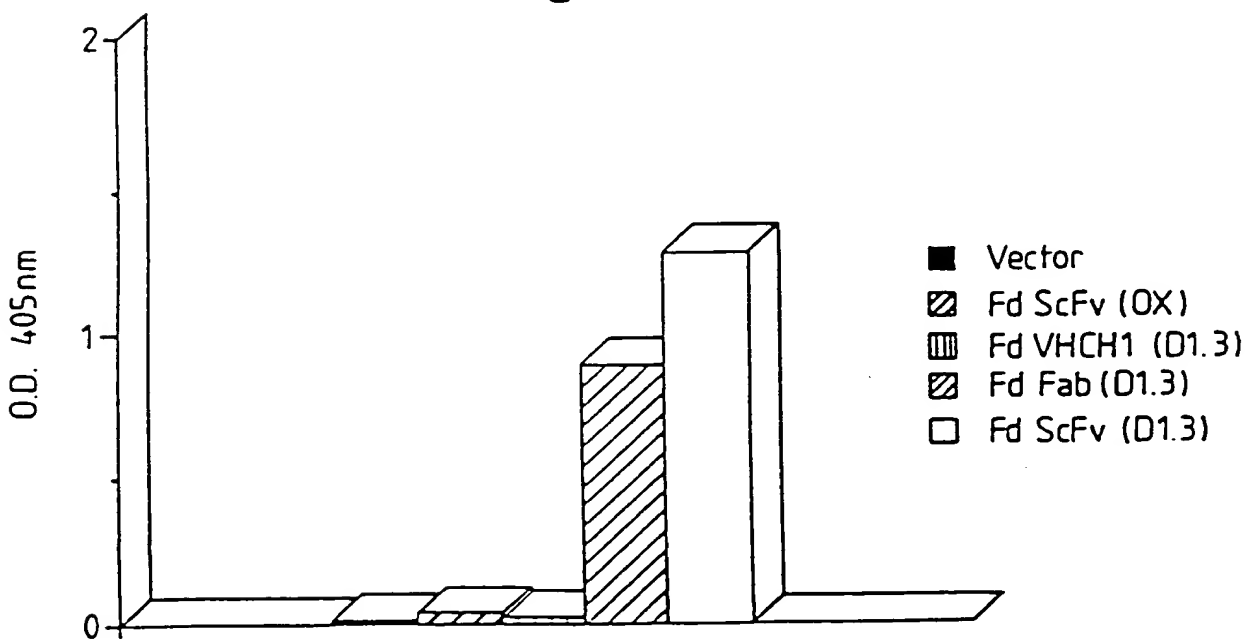


Fig.12a.

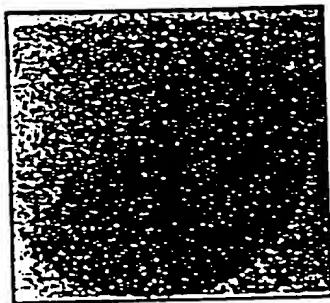


Fig.12b.

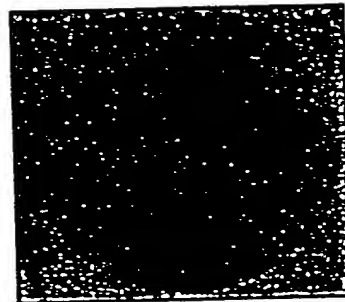


Fig.13.

Q V Q L Q E S G G G L V Q P G G
 CAG GTG CAG CTG CAG GAG TCA GGA GGA GGC TTG GTA CAG CCT GGG GGT
 PstI
 S L R L S C A T S G F T F S N Y
 TCT CTG AGA CTC TCC TGT GCA ACT TCT GGG TTC ACC TTC AGT AAT TAC
 Y M G W V R Q P P G K A L E W L
 TAC ATG GGC TGG GTC CGC CAG CCT CCA GGA AAG GCA CTT GAG TGG TTG
 G S V R N K V N G Y T T E Y S A
 GGT TCT GTT AGA AAC AAA GTT AAT GGT TAC ACA ACA GAG TAC AGT GCA
 S V K G R F T I S R D N F Q S I
 TCT GTG AAG GGG CGG TTC ACC ATC TCC AGA GAT AAT TTC CAA AGC ATC
 L Y L Q I N T L R T E D S A T Y
 CTC TAT CTT CAA ATA AAC ACC CTG AGA ACT GAG GAC AGT GCC ACT TAT
 Y C A R G Y D Y G A W F A Y W G
 TAC TGT GCA AGA GGC TAT GAT TAC GGG GCC TGG TTT GCT TAC TGG GGC
 Q G T L V T v s s g g g g s g g g g s
 CAA GGG ACC CTG GTC ACC gtc tcc tca ggtggggcggttcaggcggagggtggctct
 BstEII
 g g g g s d i E L T Q T P L S L P V
 ggcgggtggcggtcgggac atc GAG CTC ACC CAA ACT CCA CTC TCC CTG CCT GTC
 SacI
 S L G D Q A S I S C R S S Q S I
 AGT CTT GGA GAT CAA GCC TCC ATC TCT TGC AGA TCT AGT CAG AGC ATT
 V H S N G N T Y L E W Y L Q K P
 GTA CAT AGT AAT GGA AAC ACC TAT TTA GAA TGG TAC CTG CAG AAA CCA
 PstI
 G Q S P K L L I Y K V S N R F S
 GGC CAG TCT CCA AAG CTC CTG ATC TAC AAA GTT TCC AAC CGA TTT TCT
 G V P D R F S G S G S G T D F T
 GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCG GGG ACA GAT TTC ACA
 L K I S R V E A E D L G V Y Y C
 CTC AAG ATC AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT TAT TAC TGC
 F Q G S H V P Y T F G G G T K L
 TTT CAA GGT TCA CAT GTT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTC
 E I K R
GAG ATC AAA CGG (SEQ ID NO. 190)
 XhoI (SEQ ID NO. 191)

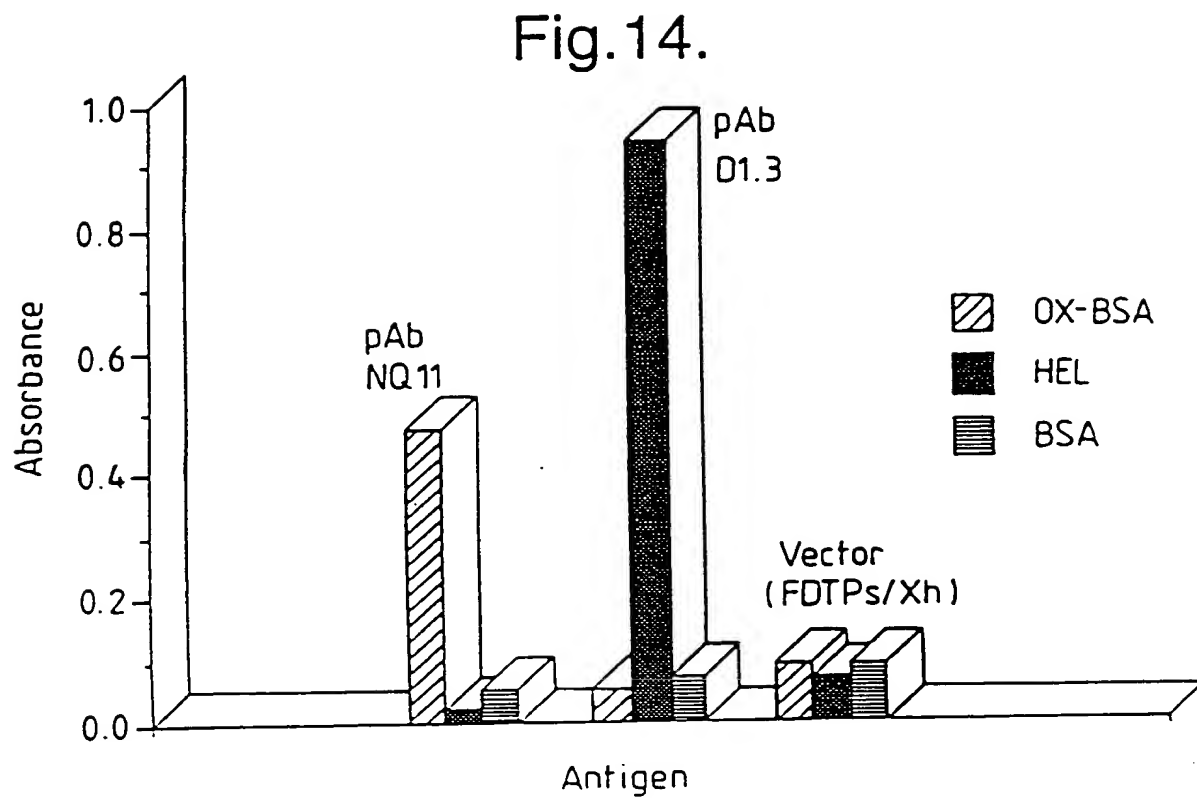


Fig.15.

5' END

R T P E M P V L (SEQ ID NO. 192)

TCT CAC AGT GCA CAA ACT GTT GAA CGG ACA CCA GAA ATG CCT GTT CTG (SEQ ID NO. 193)

ApaL1

3' END

K A A L G L K

AAA GCC GCT CTG GGG CTG AAA GCG GCC GCA GAA ACT GTT GAA AGT etc.

Not I

Fig.16 (i).

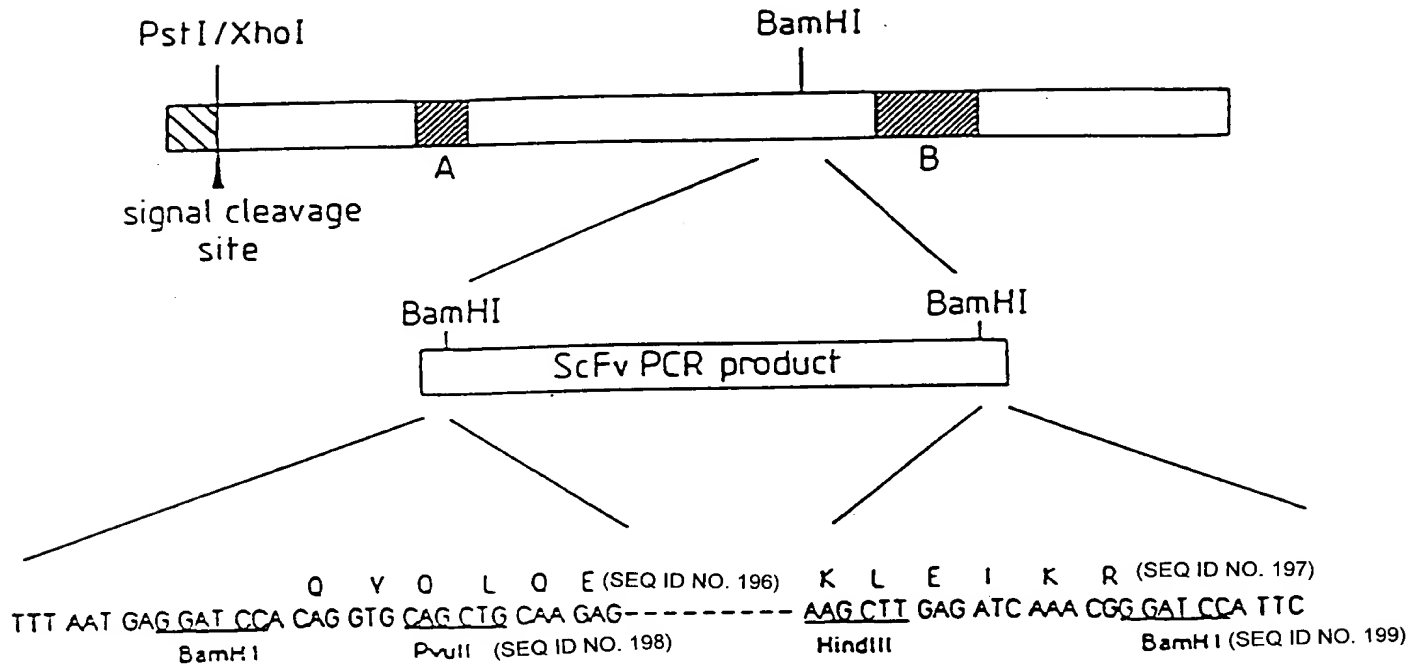


Fig.16 (ii).

A (1834) 5' GAG GGT GGT GGC TCT (SEQ ID NO. 200)
 - - -C - - (SEQ ID NO. 201)
 - - -C - - (SEQ ID NO. 202)
 - - -C - ACT 3' (1839) (SEQ ID NO. 203)

B (2284) 5' - GGC GGC GGC TCT (SEQ ID NO. 204)
 - GGT GGT GGT - (SEQ ID NO. 205)
 - - GGC GGC - (SEQ ID NO. 206)
 GAG - - GGC - (SEQ ID NO. 207)
 - - - GGT - (SEQ ID NO. 208)
 - - - GGC - (SEQ ID NO. 209)
 - - - GGT - (SEQ ID NO. 210)
 - - - GGC - 3' (2379) (SEQ ID NO. 211)

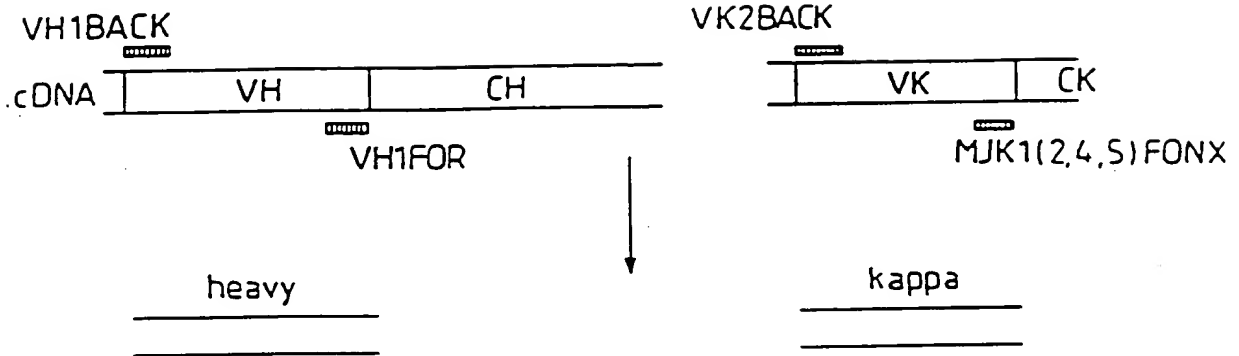
Reverse complement of mutagenic
 oligo G3Bamlink

5' GAG GGT GGC GGA TCC (SEQ ID NO. 212)

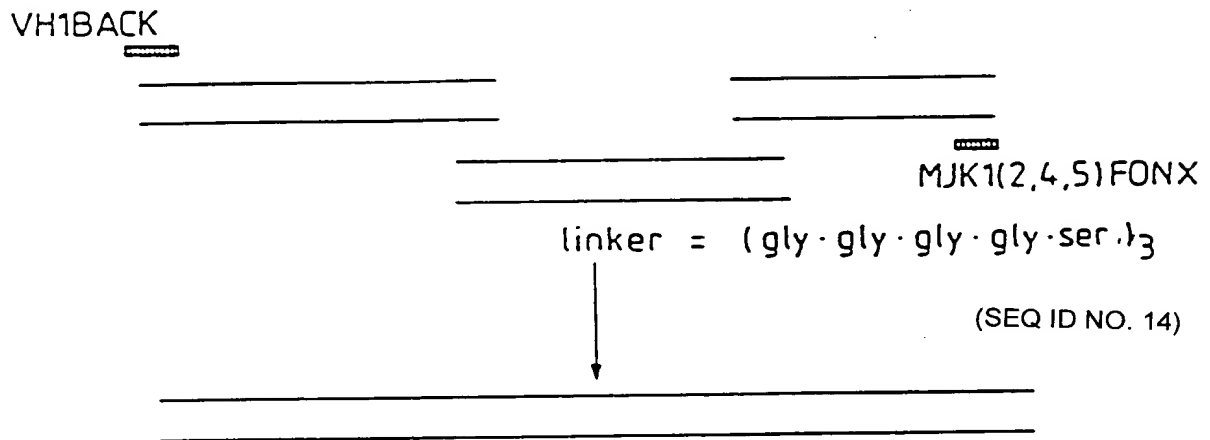
GAG GGT GGC GG 3' (SEQ ID NO. 213)

Fig.17.

1) PRIMARY PCR



2) ASSEMBLY PCR



3) ADDING RESTRICTION SITES

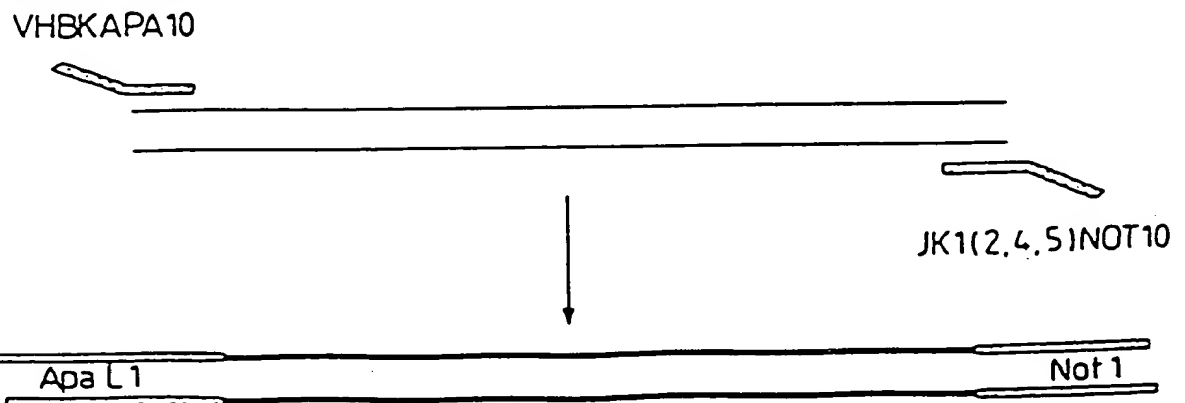


Fig.18.

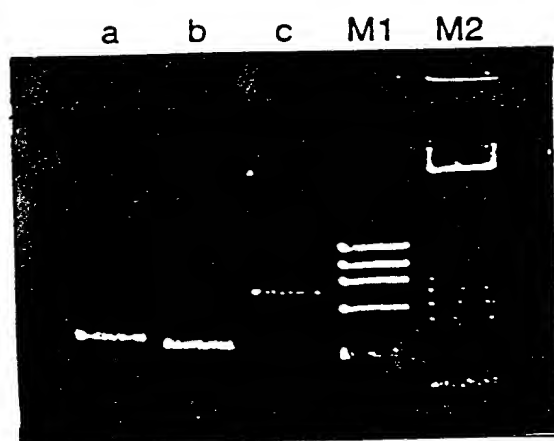


Fig.19.

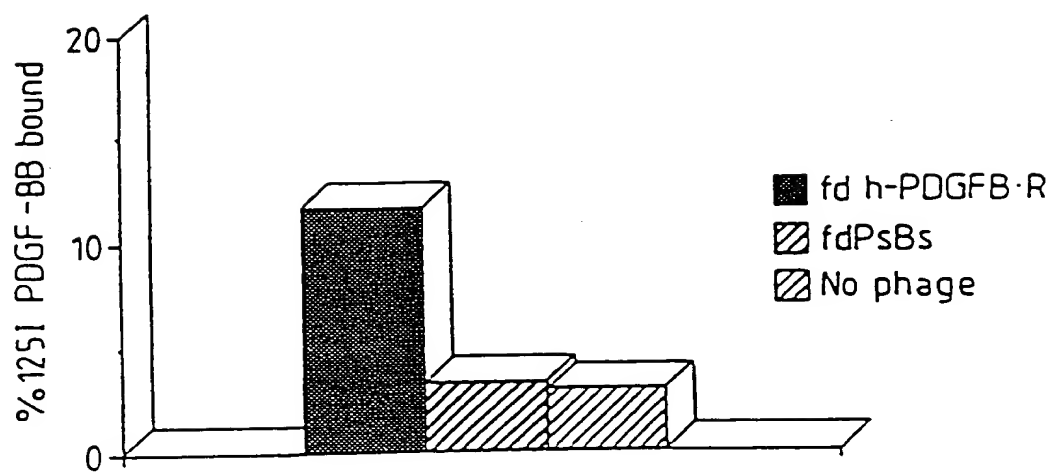
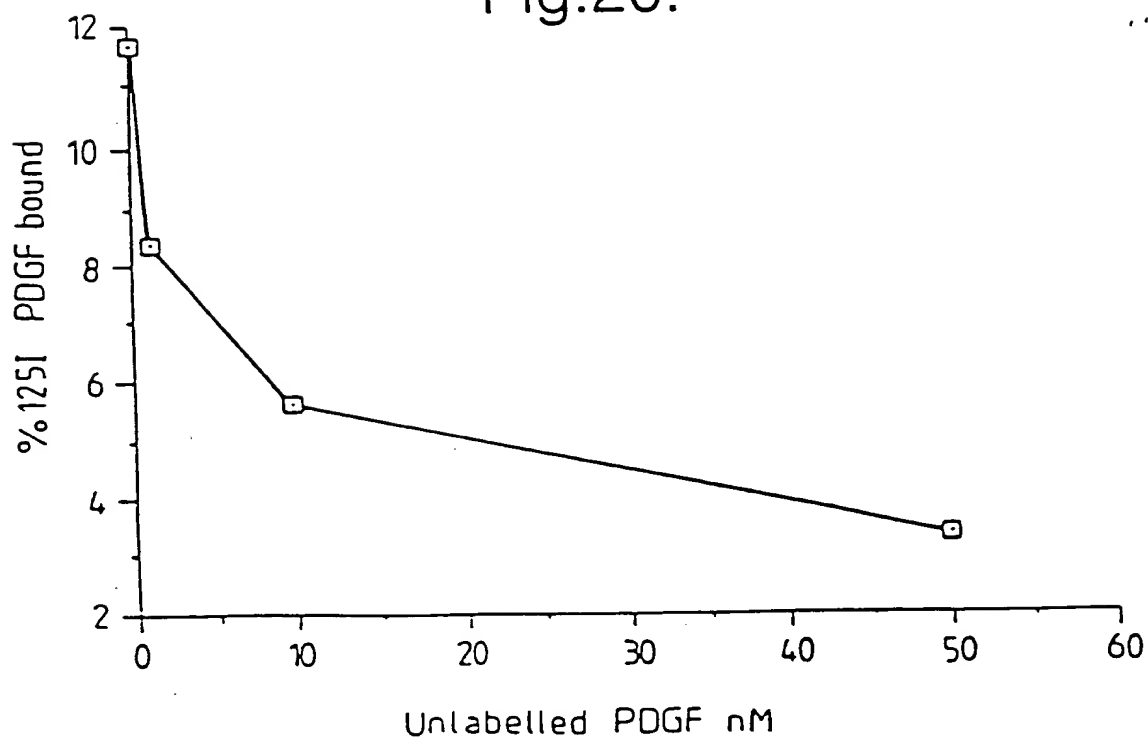


Fig.20.



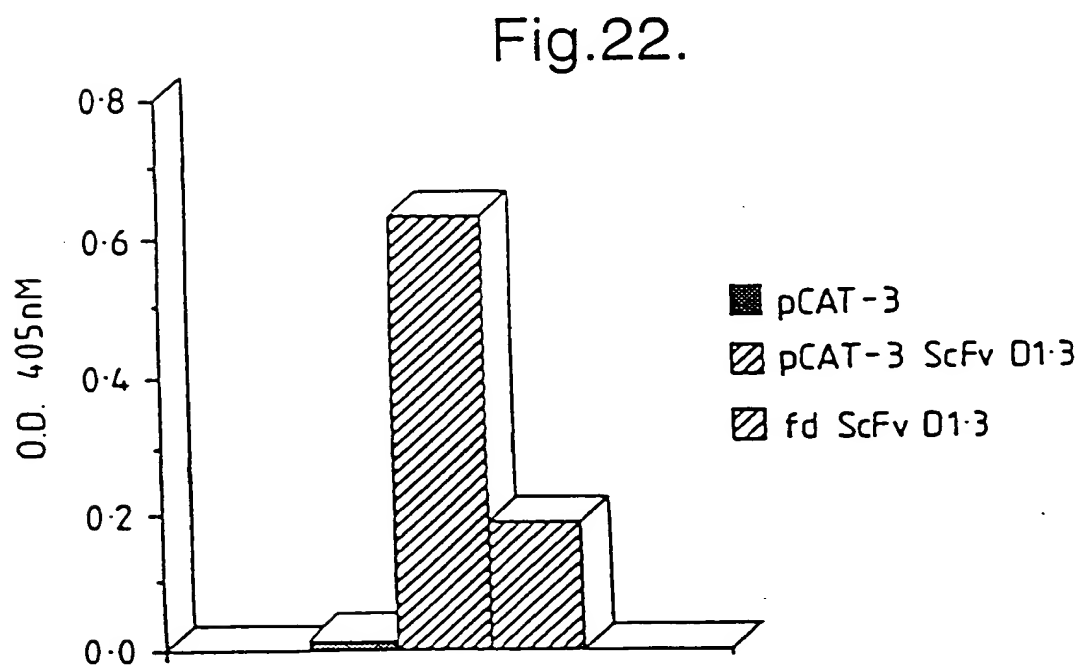
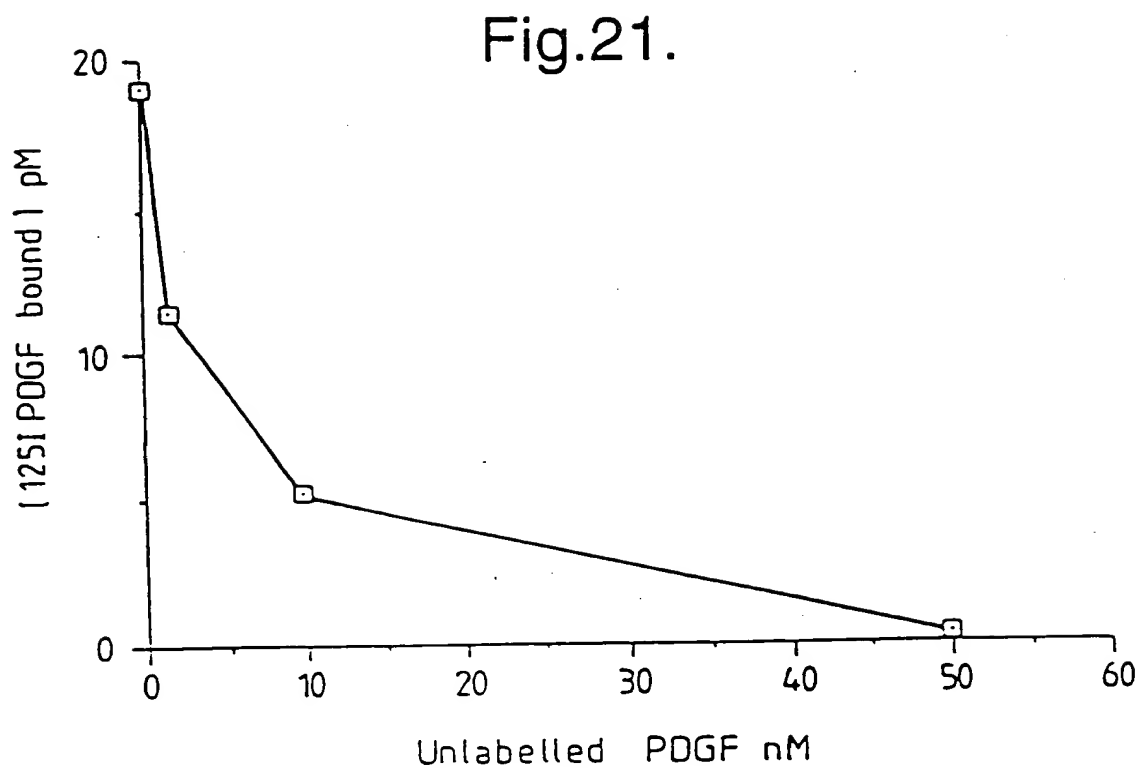


Fig.23(i)

d
M



Fig.23(ii)

M



VH sequences

Fig.24.

from combinatorial library:

	CDR1	CDR2	CDR3							
A	QVQLQSGDAELARPGASVVKHSCKASGTTT	STTHMI	WVKQRPQGGLWIG	YINPSGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAN	RYGAY	MGCGTTVTVS8	x4	1	(SEQ ID NO. 214)
B	QVQLQSGDAELARPGASVVKHSCKASGTTT	RDMMH	WVKQRPQGGLWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYCAR	NYGLY	MGCGTTVTVS8	x9	1	(SEQ ID NO. 215)
C	QVQLQSGDELVXPKA6VTVN9CKASGTTT	STVPH	WVKQRPQGGLWIG	YINPNDOTK YHEKFKD	KATLTSDK85STA YHELS6LTSEDAVYTCAL	YRFPY	MGCGTTVTVS8	x3	1	(SEQ ID NO. 216)
D	QVQLQSGDELVTRPGASVVKHSCKASGTTT	GYFPH	WVKQSHGKSLWIG	RINPNDOTFYTHNQKFKD	KATLTVDK85STAMLELSLTSEDSAVTYCVG	ITTRFAY	MGCGTTVTVS6	x3	1	(SEQ ID NO. 217)
E	QVQLQSGGPGLVNA5DSLTCTGT80FSLT	SYGMH	WVKQRPQCGGLWIG	VINAGGSTYTHNLSLHS	RLSISKDNLSQVFLKNNLSQTTDTPAMTYTCAR	URGDY	MGCGTTVTVS6		2	VIQXJ (SEQ ID NO. 218)
F	QVQLQSGDELARPGASVVKHSCKASGTTT	STLPH	WVKQRPQCGGLWIG	YINPSTGCTYTHNQKFKD	KATLTADK65SSTAYHQL68LTSEDSAVTYCAR	DYGY	MGCGTTVTVS9		1	(SEQ ID NO. 219)
G	QVQLQSGDAELVTRPGASVVKHSCKASGTTT	RYTHMI	WVKQRPQGGLWIG	YINPSTGCTYTHNQKFKD	EATLTADKSSSTA YHQL69LTSEDSAVTYCAR	DYGY	MGCGTTVTVS8		1	(SEQ ID NO. 220)
H	QVQLQSGDELAKPGASVVKLSCKASGTTT	RYTHMI	WVKQSHGKSLWIG	YINPNDGCTYTHQKFKG	KATLTVDK85SSTA YHQLSSLTSEDBAVTYCAT	DYGRD	MGCGTTVTVS6		1	(SEQ ID NO. 221)

from hierarchical library VH-rep x Vc-d:

I	QVQLQSGDAELARPGASVVKHSCKASGTTT	STVPH	WVKQSHGKSLWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	DYGY	MGCGTTVTVS9		1	(SEQ ID NO. 222)
J	QVQLQSGDAELARPGASVVKHSCKASGTTT	RYTHMI	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	DRGAY	MGCGTTVTVS6		1	(SEQ ID NO. 223)
K	QVQLQSGDAELARPGASVVKHSCKASGTTT	RDMMH	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	NYGLY	MGCGTTVTVS6	x3	1	(SEQ ID NO. 224)
L	QVQLQSGDAELARPGASVVKHSCKASGTTT	NYTHMI	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	DYGY	MGCGTTVTVS6	x2	1	(SEQ ID NO. 225)
M	QVQLQSGDAELARPGASVVKHSCKASGTTT	NYTHMI	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	DYGY	MGCGTTVTVS6		1	(SEQ ID NO. 226)
N	QVQLQSGDAELARPGASVVKHSCKASGTTT	STVPH	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	DYGY	MGCGTTVTVS6		1	(SEQ ID NO. 227)
O	QVQLQSGDAELARPGASVVKHSCKASGTTT	STVPH	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	DYGY	MGCGTTVTVS6		1	(SEQ ID NO. 228)
P	QVQLQSGDAELARPGASVVKHSCKASGTTT	STVPH	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	DYGY	MGCGTTVTVS6		1	(SEQ ID NO. 229)
Q	QVQLQSGDAELARPGASVVKHSCKASGTTT	STVPH	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	DYGY	MGCGTTVTVS6		1	(SEQ ID NO. 230)
R	QVQLQSGDAELARPGASVVKHSCKASGTTT	STVPH	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	DYGY	MGCGTTVTVS6		1	(SEQ ID NO. 231)
S	QVQLQSGDAELARPGASVVKHSCKASGTTT	STVPH	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	DYGY	MGCGTTVTVS6	x2	1	(SEQ ID NO. 232)
T	QVQLQSGDAELARPGASVVKHSCKASGTTT	STVPH	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	DYGY	MGCGTTVTVS6	x6	1	(SEQ ID NO. 233)
U	QVQLQSGDAELARPGASVVKHSCKASGTTT	STVPH	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	DYGY	MGCGTTVTVS6		1	(SEQ ID NO. 234)
V	QVQLQSGDAELARPGASVVKHSCKASGTTT	RDMMH	WVKQRPQGCGLEWIG	YINPSTGCTYTHNQKFKD	KATLTADKSSSTA YHQLSSLTSEDSAVTYTCAR	NYGLY	MGCGTTVTVS6		1	(SEQ ID NO. 235)

Fig.24 (Cont).

V_k sequences

from combinatorial library:

	CDR1	CDR2	CDR3		
a	RASQELSGYLS	WLOQKPDGSIKRLIY	AASSTLAS	GVPARFSGSRSGSGSYSLTISLSSEDFADYYC	FGACTKLEIKRA x3
b	RASSSV66SYLH	WYQKSGCASPKNMIY	BTSHLAS	GVPARFSGSGGTGYSYSLTISSVAEADAATYYC	FGACTKLEIKRA x3
c	SASSS16SNYLH	WYQKPGFSPKLLIY	RTSHLAS	GVPARFSGSGSGTYSYSLTIGTTHAEADVATYYC	FGACTKLEIKRA x3
d	SASSS16SNYLH	WYQKPGFSPKLLIS	RTSHLAG	GVPARFSGSGGTGYSYSLTIGTTHAEADVATYYC	FGACTKLEIKRA x9
e	SASSSVNTTH	WYQKPGTSPKLMIIY	STSHLAS	GVPARFSGSGSGTYSYSLTISRMEADAATYYC	FGSOTKLEIKRA x4
f	SASSSVSTN	WYQKSGTSPKRMIIY	DTSKLAS	GVPARFSGSGSGTYSYSLTISSEADAATYYC	FGSOTKLEIKRA
g	SASSSINITH	WYQKPGCASPKNMIY	DTSKLAS	GVPARFSGSGSGTYSYSLTISSEADAATYYC	FGSOTKLEIKRA

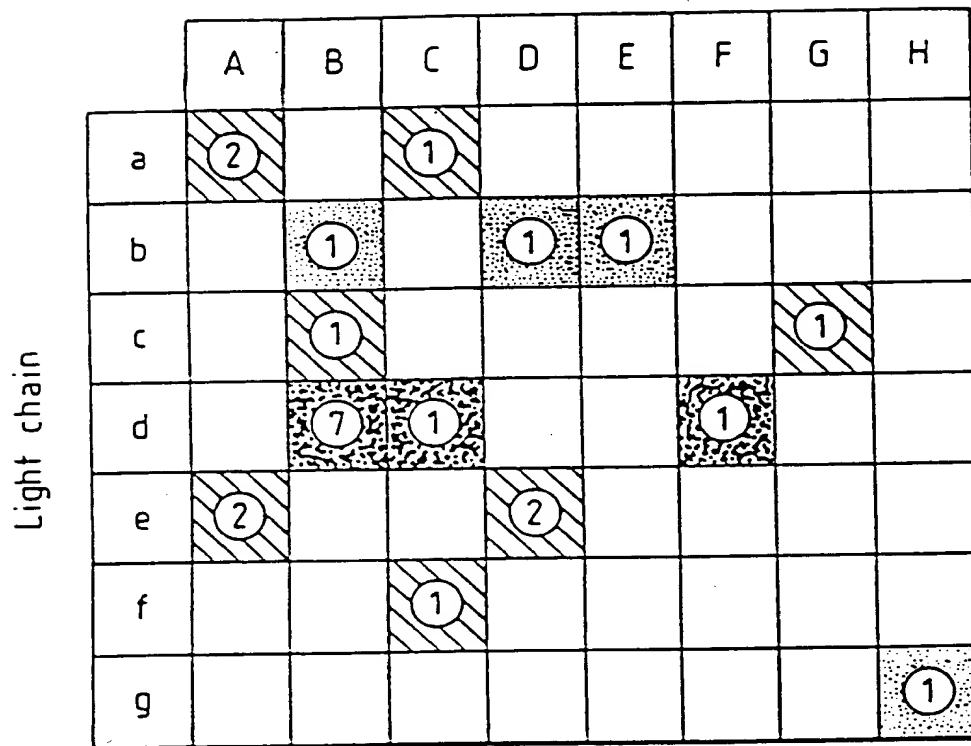
from hierarchical library VH-B x V_k-rep:

	CDR1	CDR2	CDR3		
h	SASSSVSTDI	WYQKSGTSPKRMIIY	DTSKLAG	GVPARFSGSGSGTYSYSLTISSEADAATYYC	FGACTKLEIKRA x4
i	SASSSV6YIH	WYQKPGTSPKLMIIY	STSHLAG	GVPARFSGSGSGTYSYSLTISSEADAATYYC	FGACTKLEIKRA
j	SASSS16SNYLH	WYQKPGFSPKLLIY	RTSHLAS	GVPARFSGSGSGTYSYSLTIGTTHAEADVATYYC	FGGTTKLEIKRA
k	SATS61SSNITH	WYQKPGFSPKLLIY	RTSHLAS	GVPARFSGSGSGTYSYSLTIGTTHAEADVATYYC	FGGTTKLEIKRA
l	SASSS16SNYLH	WYQKPGFSPKLLIY	RTSHLAS	GVPARFSGSGSGTYSYSLTIGTTHAEADVATYYC	FGGTTKLEIKRA
m	SASSS16SNYLH	WYQKPGFSPKLLIY	RTSHLAG	GVPARFSGSGSGTYSYSLTIGTTHAEADVATYYC	FGGTTKLEIKRA
n	SASSS16SNYLH	WYQKPGFSPKLLIY	RTSHLAS	GVPARFSGSGSGTYSYSLTIGTTHAEADVATYYC	FGGTTKLEIKRA
o	SASSS16SNYLH	WYQKPGFSPKLLIY	RTSHLAG	GVPARFSGSGSGTYSYSLTIGTTHAEADVATYYC	FGGTTKLEIKRA
p	SASSSV6YIH	WYQKSGTSPKRMIIY	DTSKLAG	GVPARFSGSGSGTYSYSLTISSEADAATYYC	FGGTTKLEIKRA x3
q	SASSSV6YIH	WYQKSGTSPKRMIIY	DTSKLAG	GVPARFSGSGSGTYSYSLTISSEADAATYYC	FGGTTKLEIKRA
r	SASSSV6YIH	WYQKSGASPKNMIY	STSHLAG	GVPARFSGSGSGTYSYSLTISSEADAATYYC	FGGTTKLEIKRA
s	RASSSV6YIH	WYQKSGASPKNMIY	STSHLAG	GVPARFSGSGSGTYSYSLTISSEADAATYYC	FGGTTKLEIKRA
t	RASSSV6YIH	WYQKSGASPKNMIY	STSHLAG	GVPARFSGSGSGTYSYSLTISSEADAATYYC	FGGTTKLEIKRA
u	RASSSV6YIH	WYQKSGASPKNMIY	STSHLAG	GVPARFSGSGSGTYSYSLTISSEADAATYYC	FGGTTKLEIKRA
v	RASSSV6YIH	WYQKSGASPKNMIY	STSHLAG	GVPARFSGSGSGTYSYSLTISSEADAATYYC	FGGTTKLEIKRA
w	SASSS16SNYLH	WYQKPGFSPKLLIY	RTSHLAG	GVPARFSGSGSGTYSYSLTIGTTHAEADVATYYC	FGGTTKLEIKRA

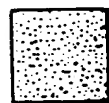
(SEQ ID NO. 243)
(SEQ ID NO. 244)
(SEQ ID NO. 245)
(SEQ ID NO. 246)
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(SEQ ID NO. 248)
(SEQ ID NO. 249)
(SEQ ID NO. 250)
(SEQ ID NO. 251)
(SEQ ID NO. 252)
(SEQ ID NO. 253)
(SEQ ID NO. 254)
(SEQ ID NO. 255)
(SEQ ID NO. 256)
(SEQ ID NO. 257)
(SEQ ID NO. 258)

Fig.25.

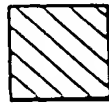
HEAVY CHAIN



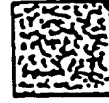
OD_{405nm} in ELISA



0.2 - 0.9



0.9 - 2.0



>2.0

Fig.26(a).

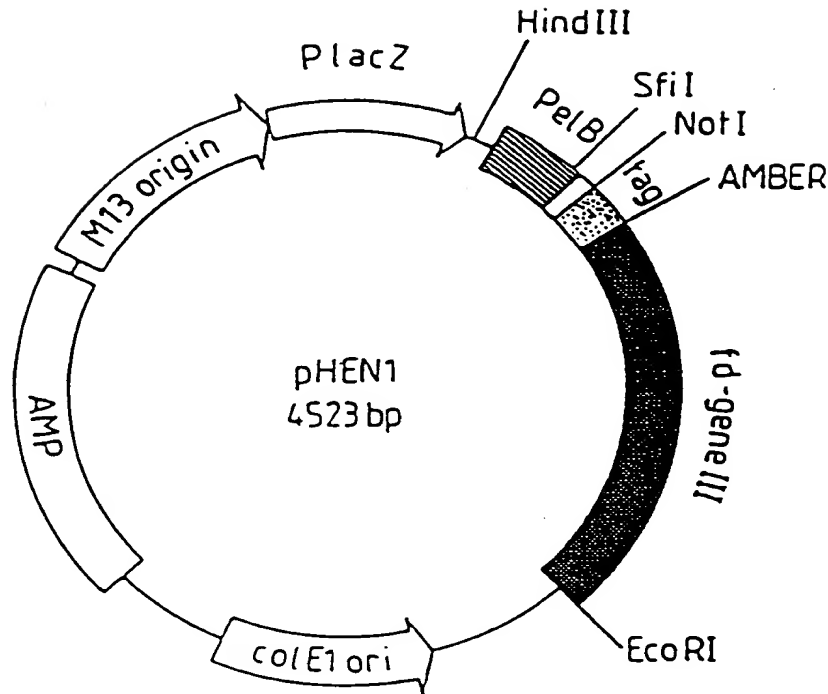
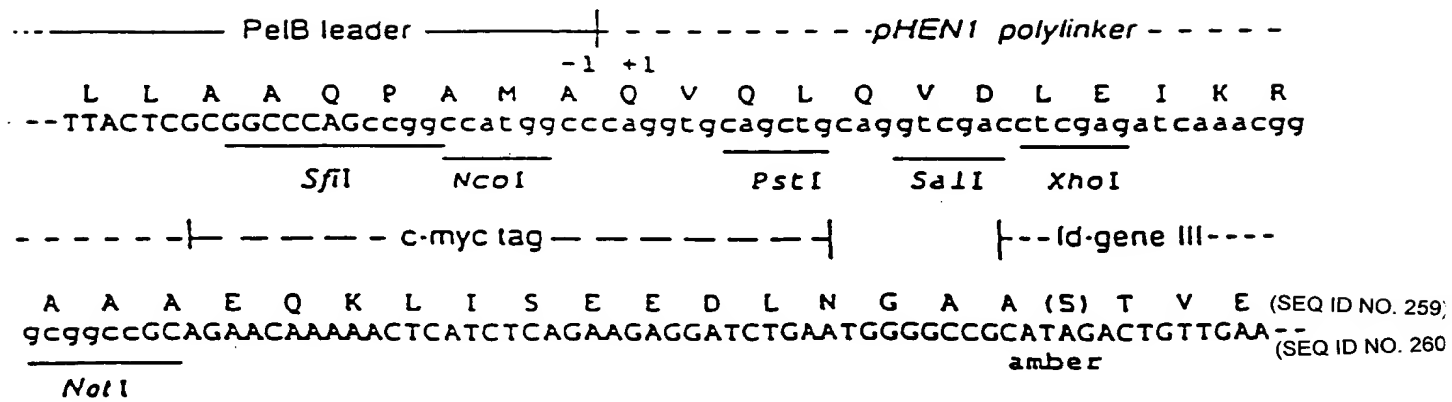


Fig.26(b).



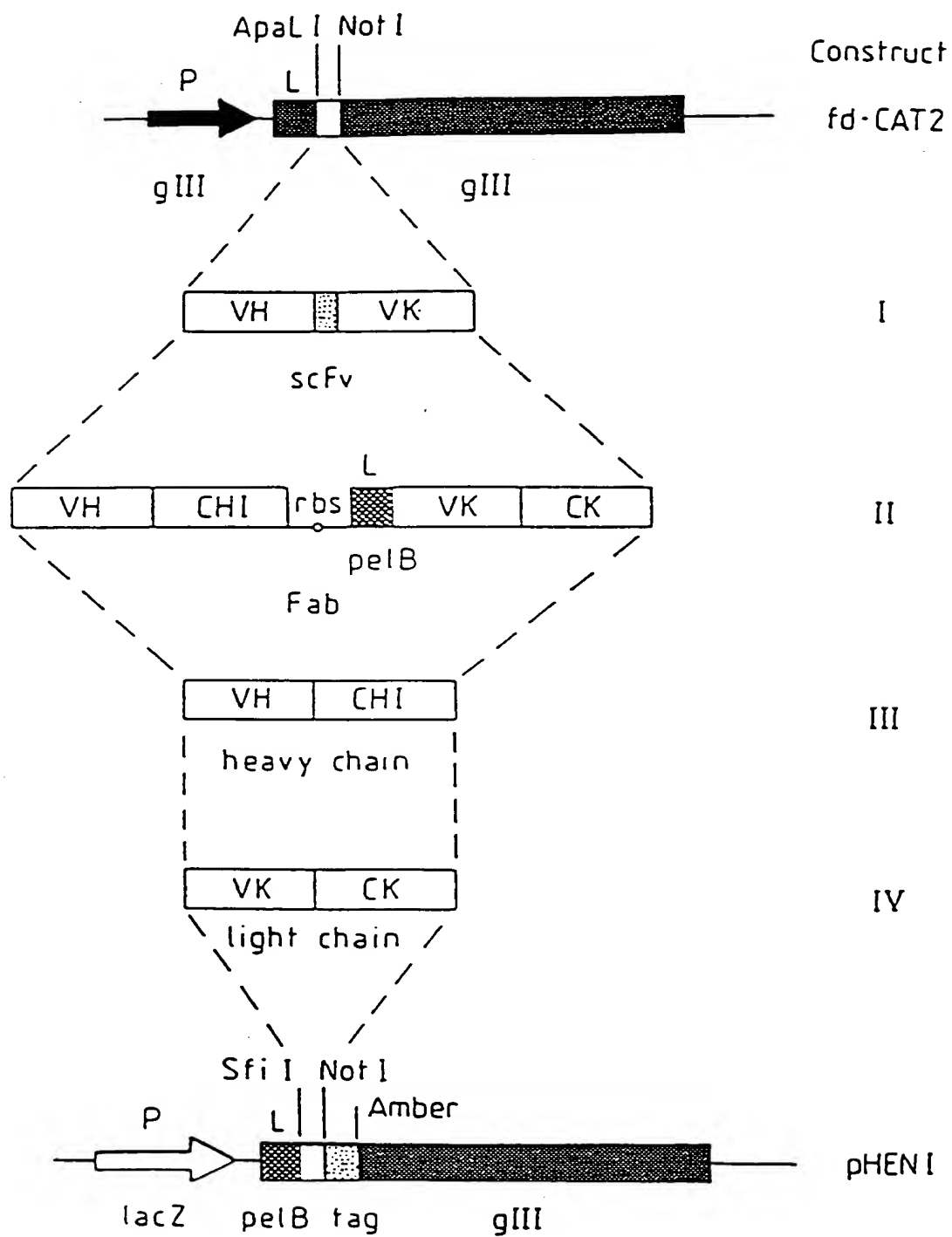


Fig.28.

Fab

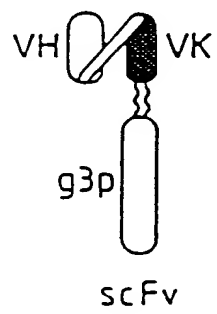
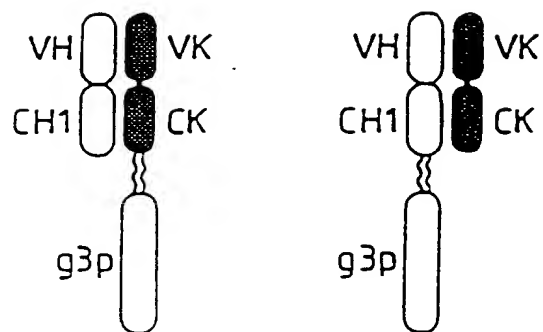


Fig.29.

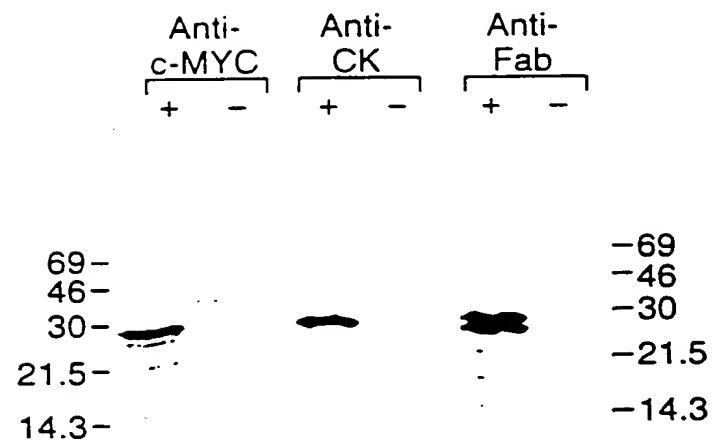


Fig.30.

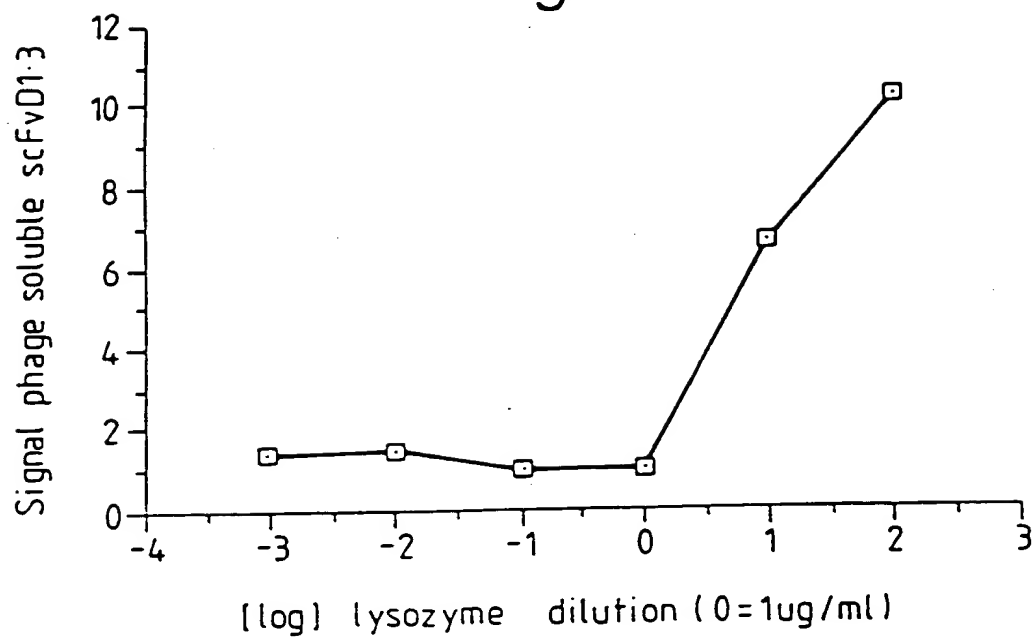


Fig.31.

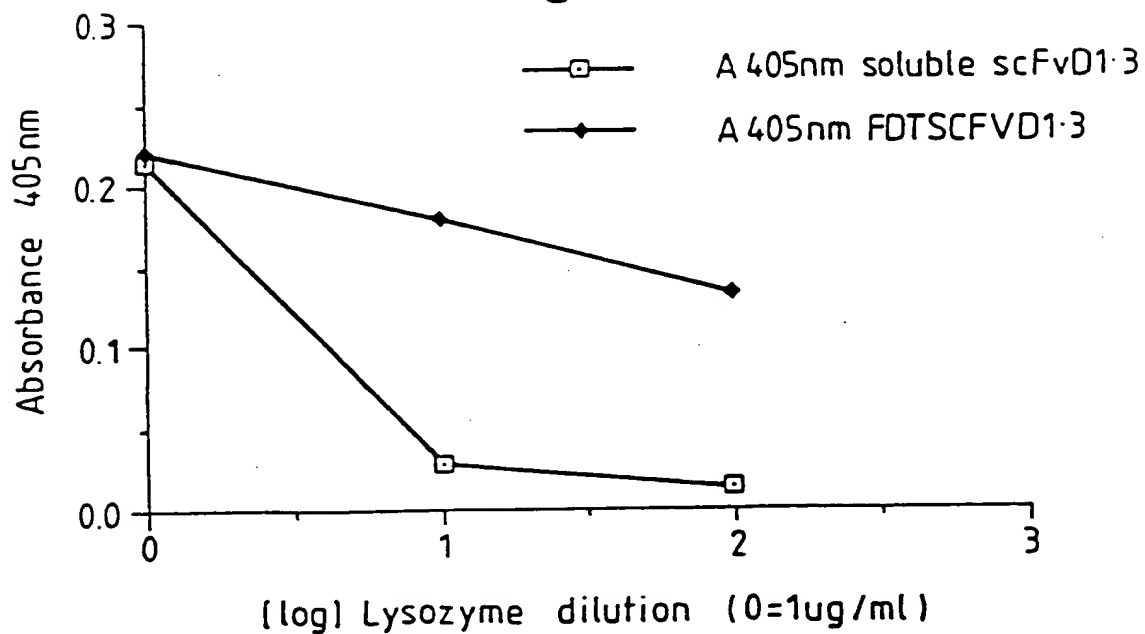


Fig.32.

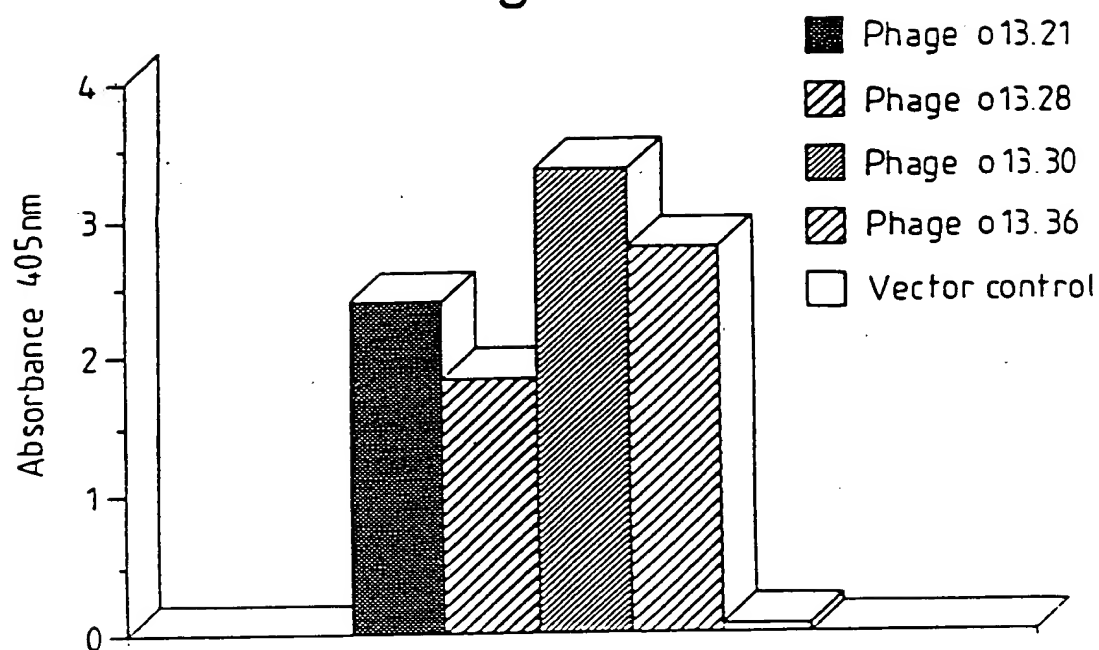


Fig.33.

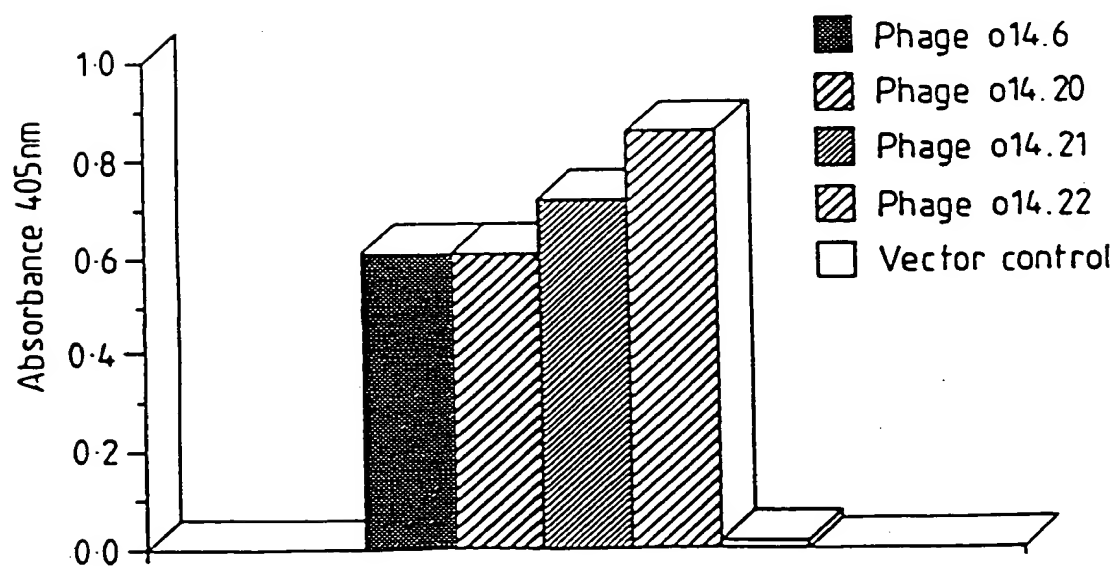


Fig.34.

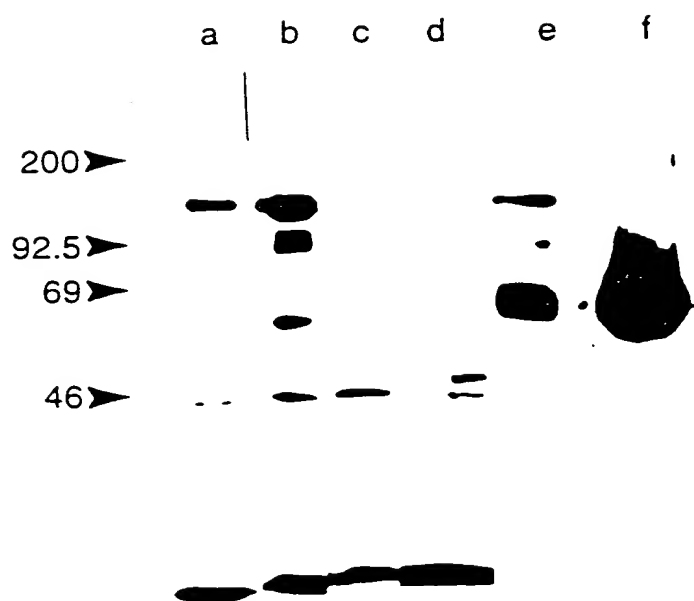


Fig.35A.

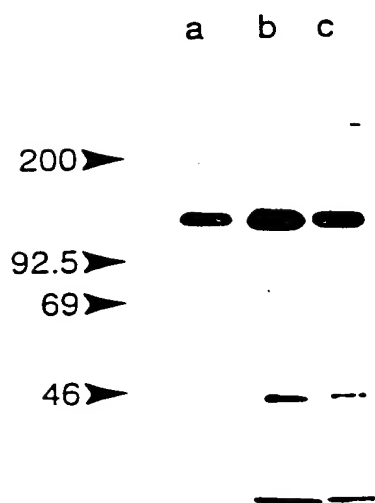


Fig.35B.

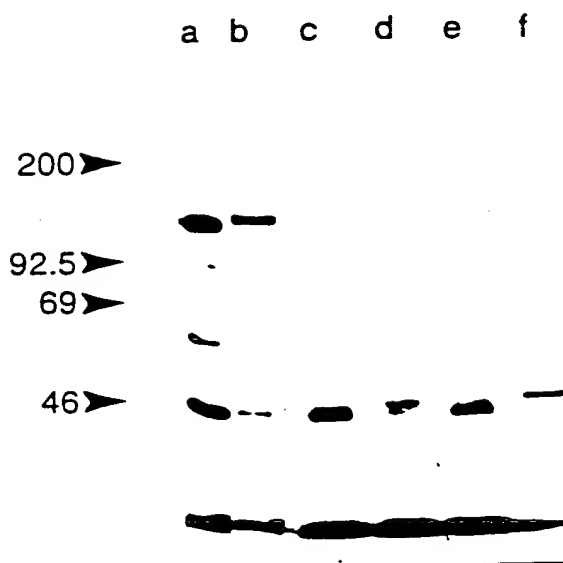


Fig.36.

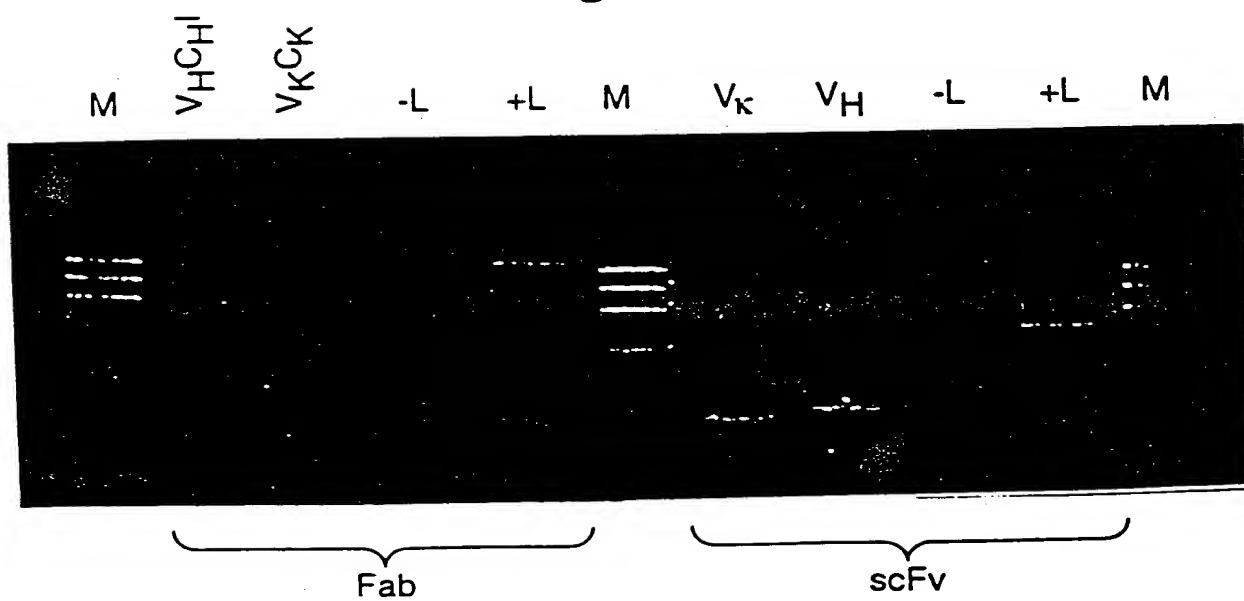


Fig.37.

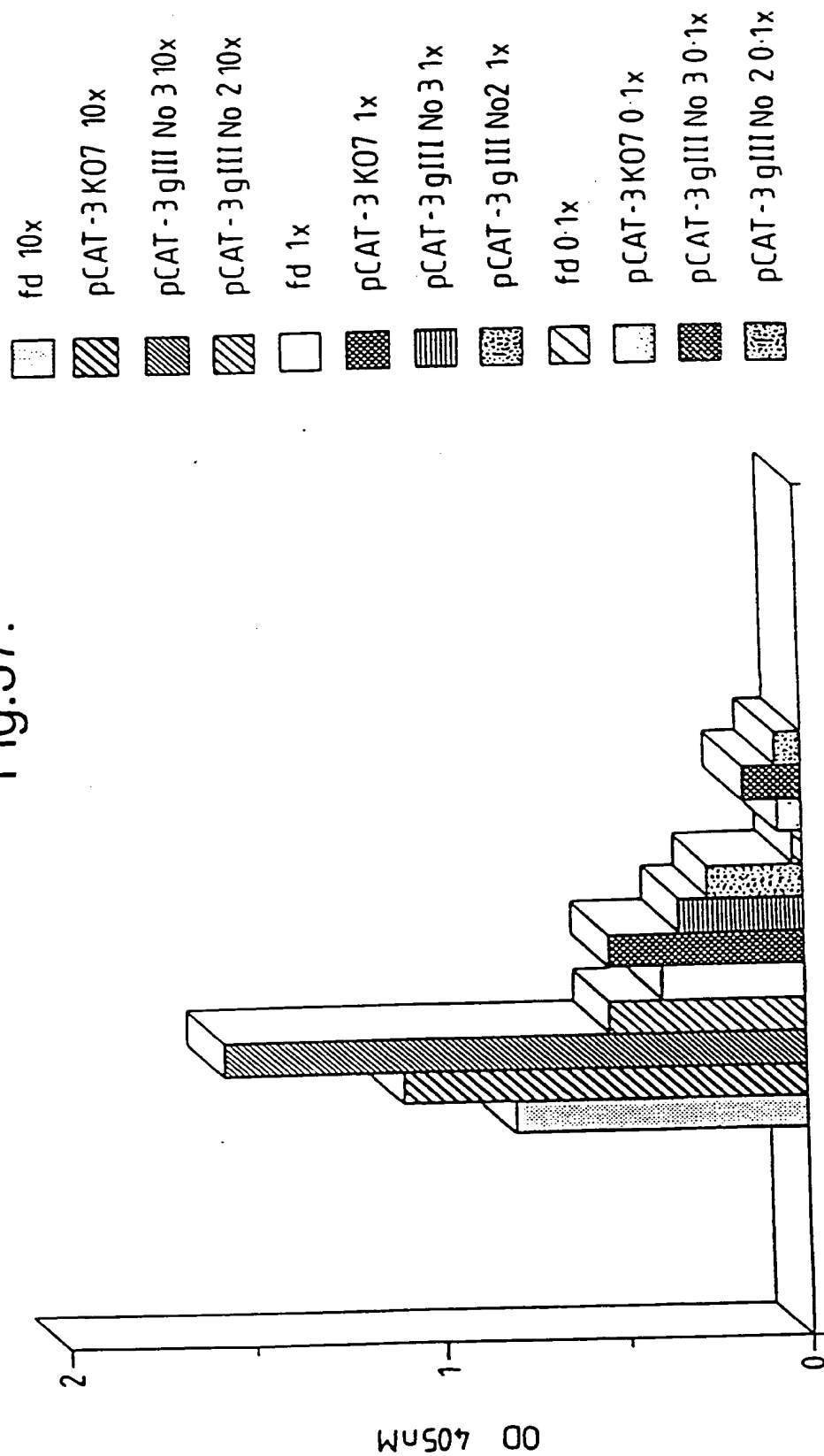


Fig.38A.

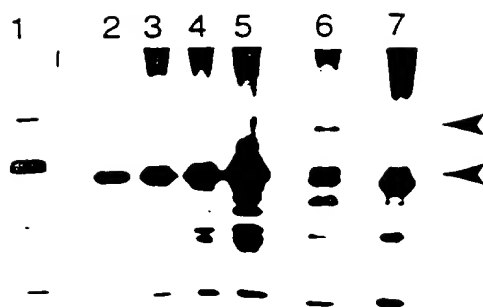


Fig.38B.

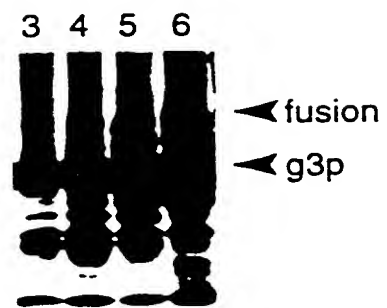


Fig.39.

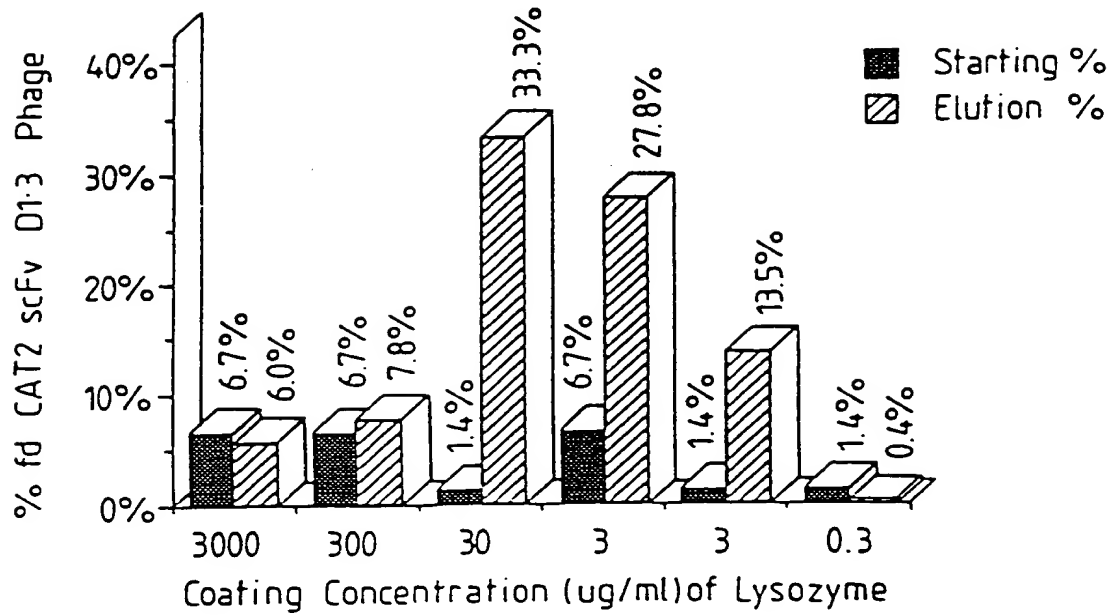


Fig.40.

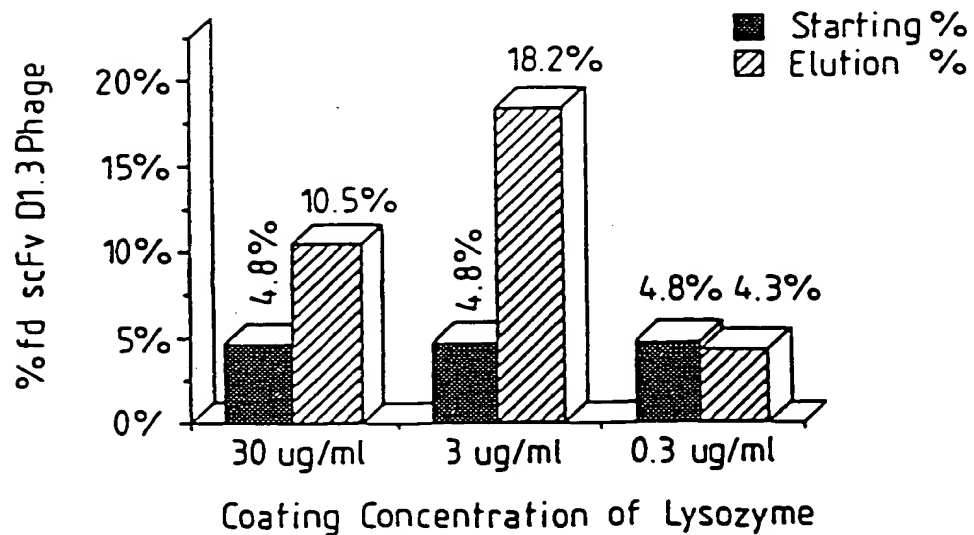


Fig.41.

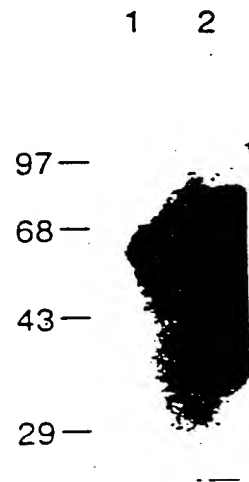


Fig.42.

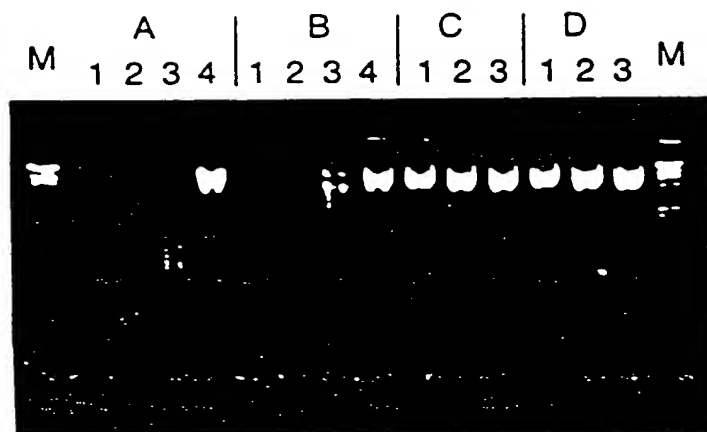


Fig.43.

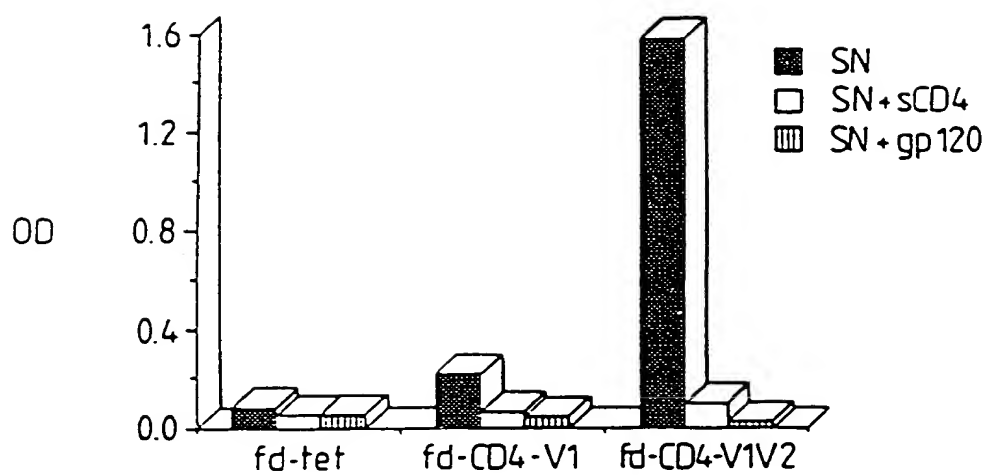


Fig.44 (i).

10 20 30 40 50 60 70 80 90
 TTCTATTCTCAGTGCNCAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTGAAGCTGTCTCCTGCAAGGCT
 AAGATAAGAGTGTACGTGTCAGGTCGACGTCGTGCAGACCCCGACTCGAACACTTCGGACCCCGAAGTCACTTCGACAGGACGTTCGGA
 PheTyrSerHisSerAlaGlnValGlnLeuGlnSerGlyAlaGluLeuValLysProGlyAlaSerValLysLeuSerCysLysAla
 100 110 120 130 140 150 160 170 180
 TCTGGCTACACCTTCACCAGCTACTGGATGCACCTGGGTGAAGCAGAGGCCCTGGACGAGCCCTTGAGTGGATTGGAAGGATTGATCCTAAT
 AGACCGATGTGGAAGTGGTCGATGACCTACGTGACCCACTTCGTCTCCGACCTGCTCCGGAACCTCACCTAACCTTCCTAACTAGGATTA
 SerGlyTyrThrPheThrSerTyrTrpMetHisTrpValLysGlnArgProGlyArgGlyLeuGluTrpIleGlyArgIleAspProAsn
 190 200 210 220 230 240 250 260 270
 AGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAACCCCTCCAGCACAGCCTACATGCAGCTCAGC
 TCACCAACCATGATTCACTTCAAGTTCCTCGTTCGGGTGACCTGACATCTGTTGGAGGTGCTGTCGGATGTACGTCGAGTCG
 SerGlyGlyThrLysTyrAsnGluLysPheLysSerLysAlaThrLeuThrValAspLysProSerSerThrAlaTyrMetGlnLeuSer
 280 290 300 310 320 330 340 350 360
 AGCCTGACATCTGAGGACTCTCGGTCTATTATTGTGCAAGNTACGACTACGGTAGTAGCTACTACTTTGACTACTGGGGCCAAAGGGACC
 TCGGACTGTAGACTCCTGAGACGCCAGATAATAACACGTTCTATGCTGATGCCATCATCGATGATGAACTGATGACCCCGGTTCCTCTGG
 SerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgTyrAspTyrGlySerSerTyrTyrPheAspTyrTrpGlyGlnGlyThr
 370 380 390 400 410 420 430 440 450
 ACGGTCACCGTCTCCTCNGGTGGAGGCGGTTACAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCAGGCTGTGGGACACAGGAATCTGCA
 TGCCAGTGGCAGAGGATCCACCTCCGCCAAGTCCGCCCTCCACGAGACCGCACCGCTAGGTCCGACACACCCCTGTGTCTTAGACGT
 ThrValThrValSerSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlnAlaValGlyThrGlnGluSerAla
 460 470 480 490 500 510 520 530 540
 CTCACCACATCACCTGGTGAACAGTCACACTCTGTGCGCTCAAGTACTGGGGCTGTTACAACACTAGTAACATATGCCAACCTGGGTCCAA
 GAGTGGTGTAGTGACCACTTTGTGTCAGTGTGAGTGAACAGCGAGTTTCATGACCCCGACAAATGTTGATCATTTGATACGGTTGACCCCAAGTT
 LeuThrThrSerProGlyGluThrValThrLeuThrCysArgSerSerThrGlyAlaValThrThrSerAsnTyrAlaAsnTrpValGln
 550 560 570 580 590 600 610 620 630
 GAAAAACAGATCATTTATTCACCTGGTCTAATAGGTGGTACCAACAACCGAGCTCCAGGTGTTCTGCCAGATTCTCAGGCTCCCTTGATT
 CTTTGTGGTCTAGTAAATAAGTGACCAGATTATCCACCATGTTGTTGGCTCGAGGTCCACAAAGGACGGTCTAAGAGTCCGAGGGACTAA
 GluLysProAspHisLeuPheThrGlyLeuIleGlyGlyThrAsnAsnArgAlaProGlyValProAlaArgPheSerGlySerLeuIle

Fig.44 (ii).

640 650 660 670 680 690 700 710 720
GGAGACAAGGCTGCCCTCACCATCACAGGGGCGCACAGACTGAGGATGAGGCATATATTTCTGTGCTCTATGGTACAGCAACCATTTGGGTG
CCTCTGTTCCGACGGAGTGGTAGTGTCCTGCTGACTCCTACTCCGTTATATAAGACACGAGATACCATGTGCGTTGGTAACCCAC
GlyAspLysAlaAlaLeuThrIleThrGlyAlaGlnThrGluAspGluAlaIleTyrPheCysAlaLeuTrpTyrnberAsnHisTrpVal
730 740 750 760 770
TTCGTTGGAGGAAACAACTGACTGTCCCTCGAGATCAACGGGGCGCGC (SEQ ID NO. 261)
AAGCCACCTCCTTGGTTTGACTGACAGGAGCTCTAGTTGCCCGCCGGCG
PheGlyGlyGlyThrLysLeuThrValLeuGluIleLysArgAlaAla (SEQ ID NO. 262)



Fig.45.

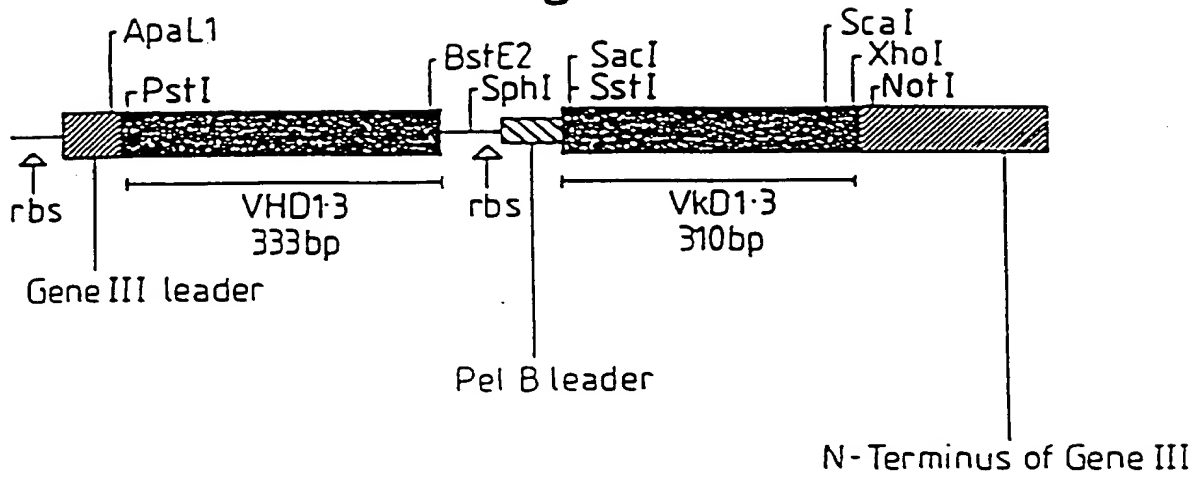


Fig.46.

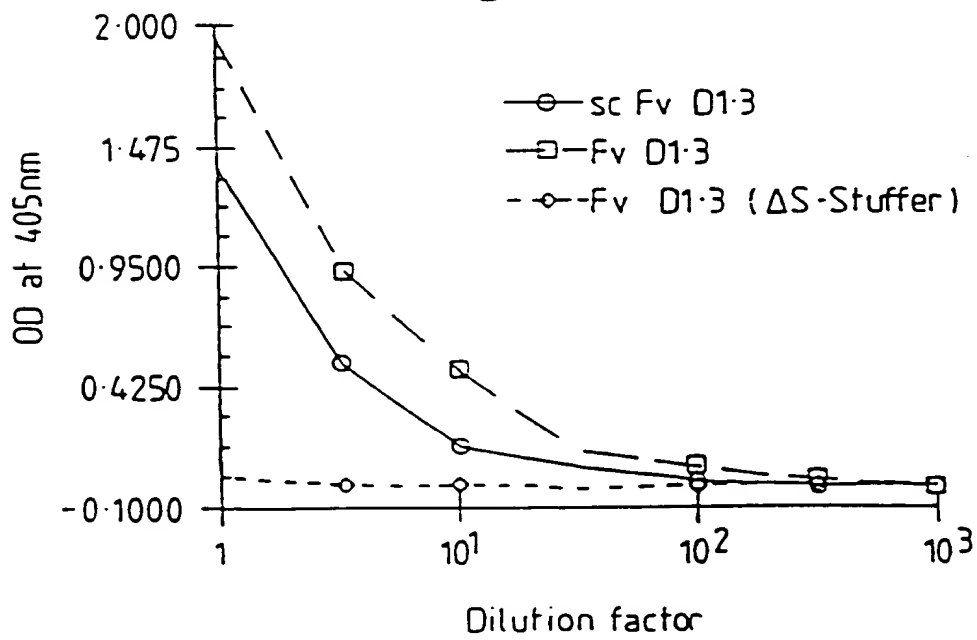


Fig.47.

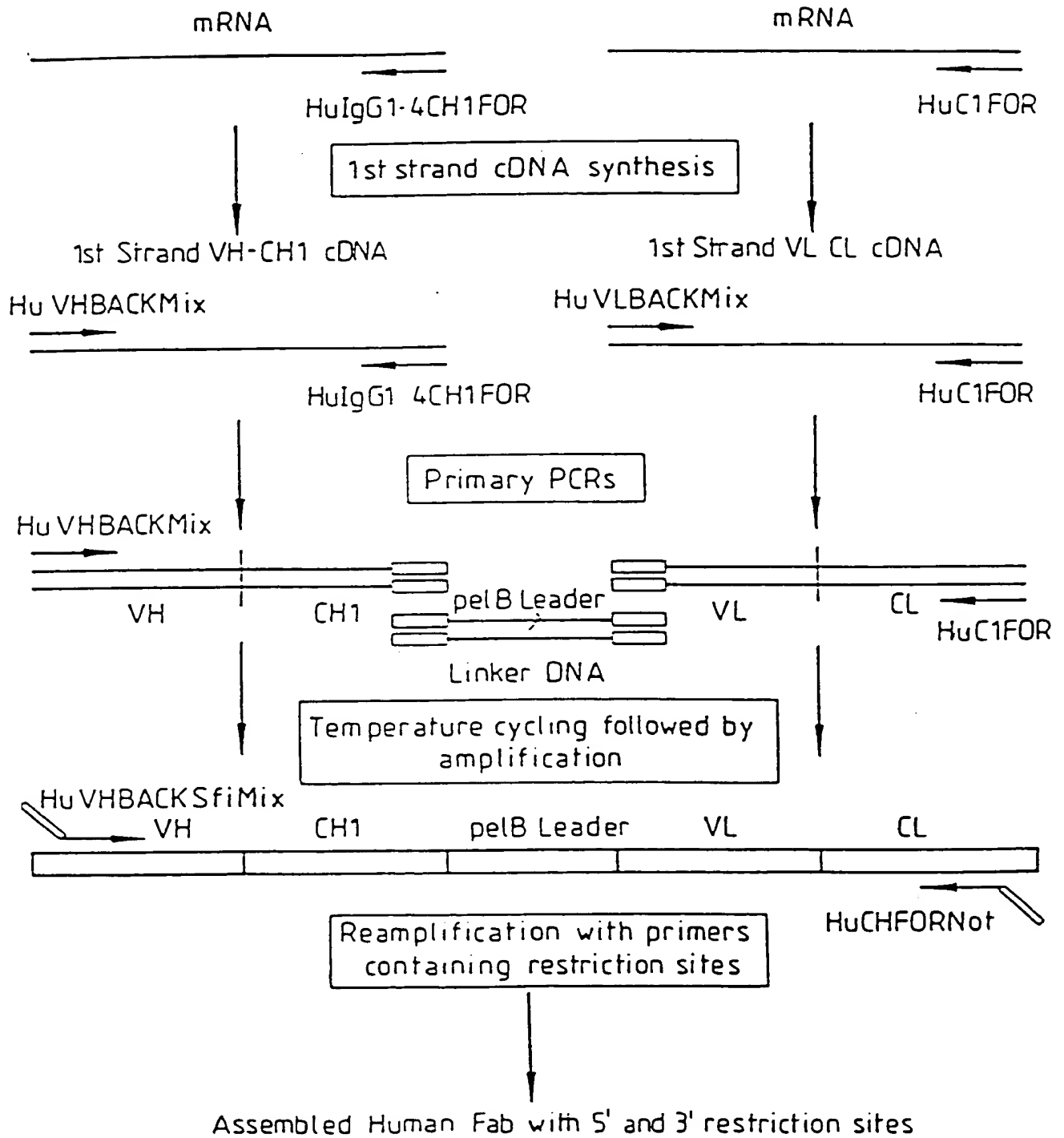


Fig.48(i)

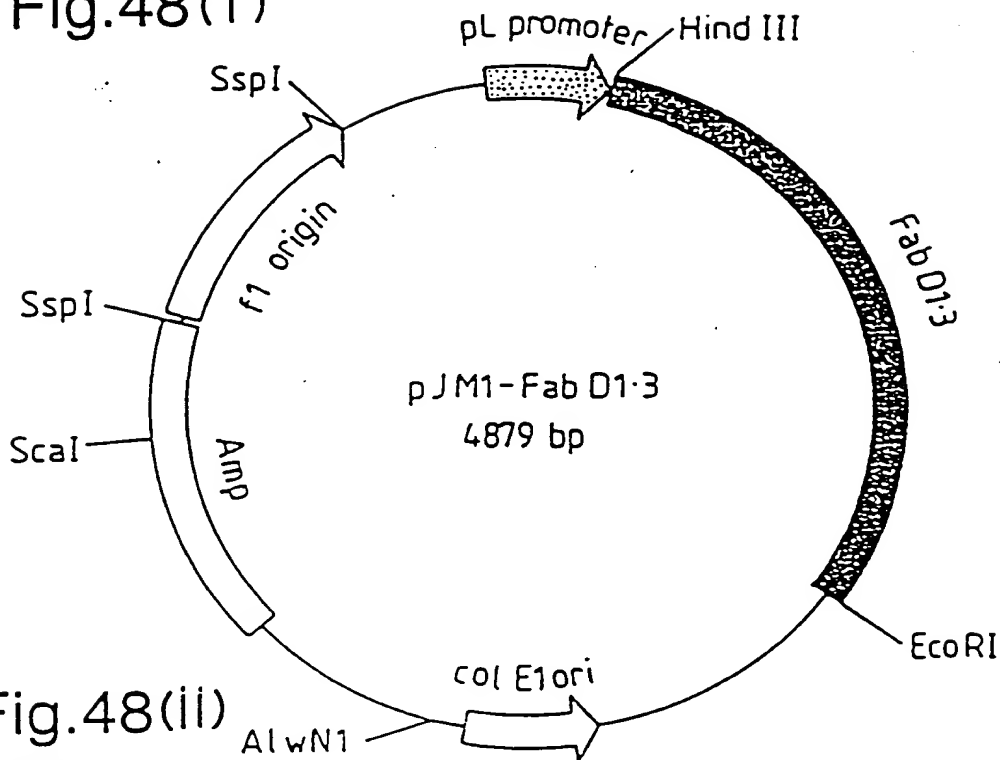


Fig.48(ii)

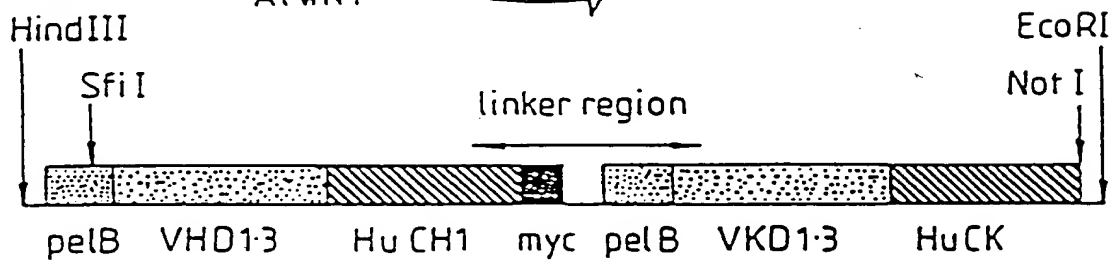


Fig.48(iii)

← 3' Human CH1 and hinge →
 K P S N T K V D K K V E P K S S T K T H T
 AACCCAGCAACACCAAGGTCGACAAGAAAGTTGAGCCCAAATCTTCAACTAAGACGCACACA

→ myc peptide tag →
 S G G E Q K L I S E E D L N * *
 TCAGGAGGTGAACAGAAGCTCATCTCAGAAGAGGATCTGAATTAATAAGGGAGCTTGCATGCA

(SEQ ID NO. 263)

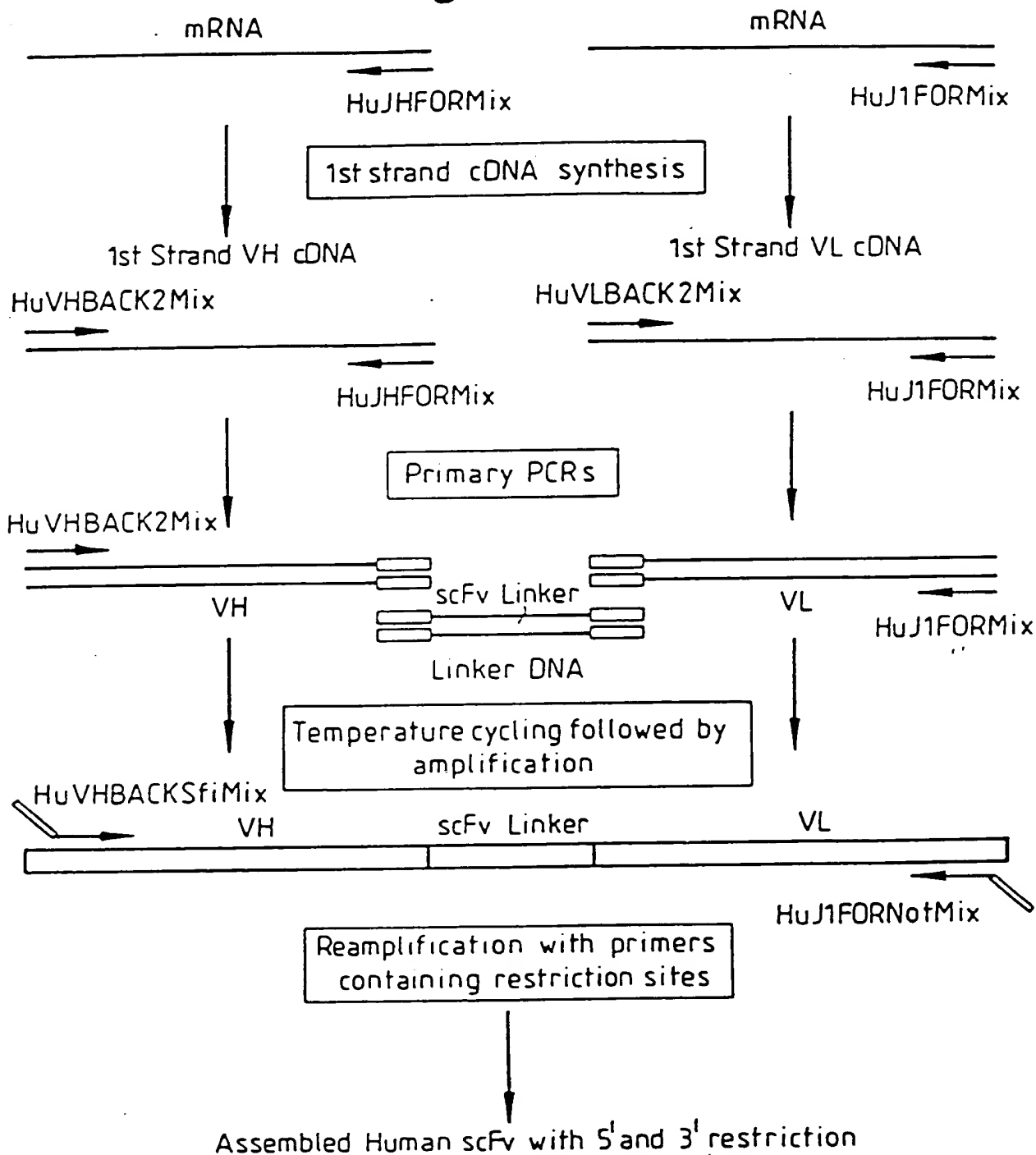
← pelB leader →
 M K Y L L P T A A A G L
 AATTCTATTTCAGGAGACAGTCATAATGAATAACCTATTGCCTACGGCAGCCGCTGGATTGT

→ 5' Vk →
 L L P A A Q P A M A D I E L T Q S P
 TATTACCTGCTGCCCAACCAGOGATGGGCGACATOGAGTTACCCAGTCTCC

(SEQ ID NO. 264)

(SEQ ID NO. 265)

Fig.49.



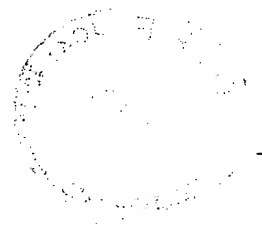


Fig.50(i)

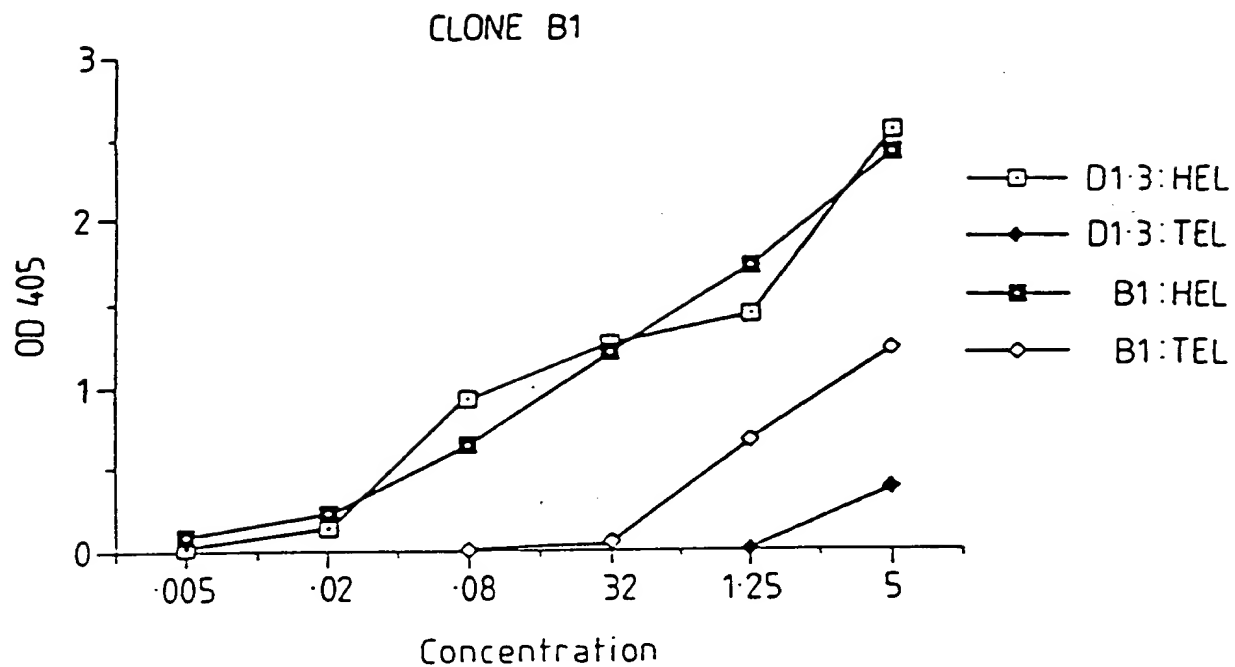
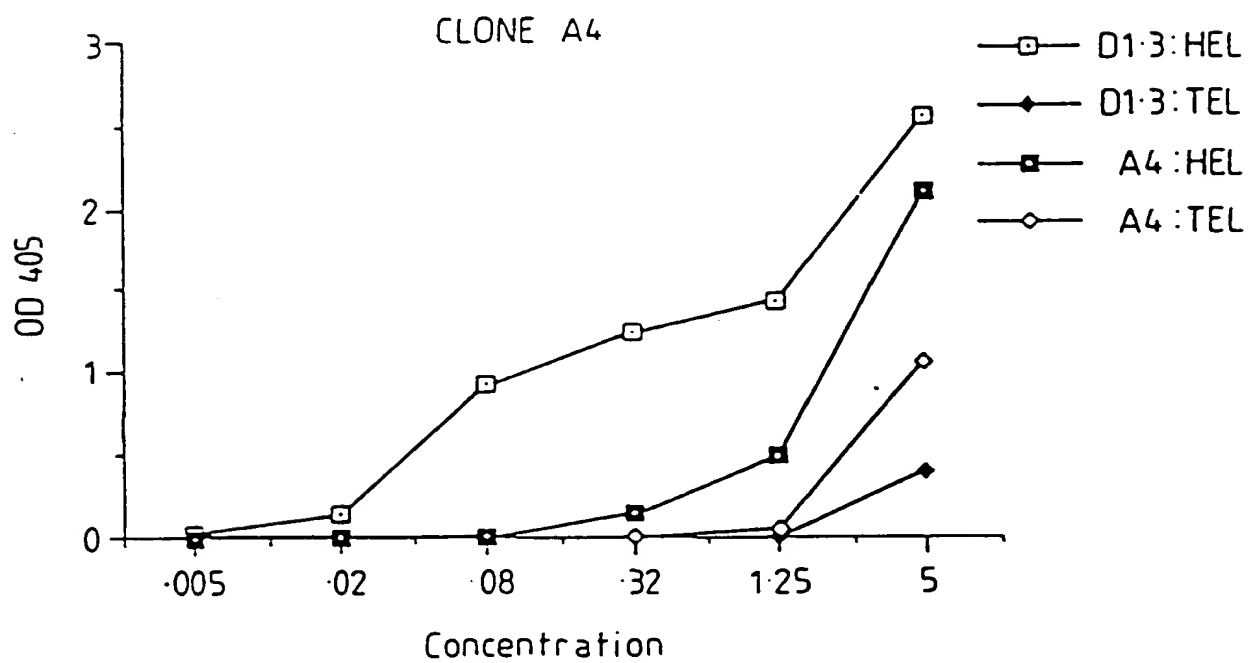


Fig.50(ii)



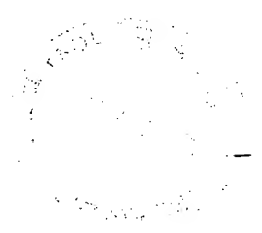


Fig.51.

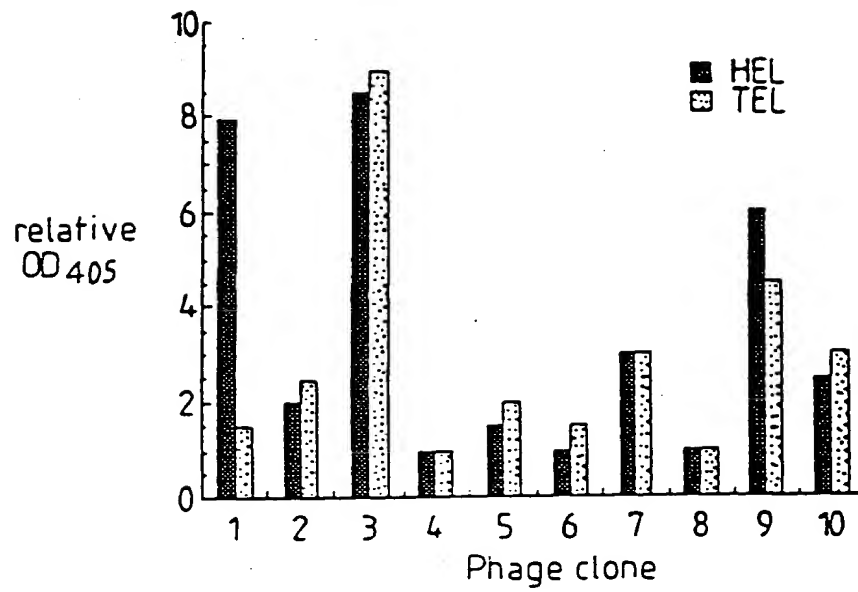


Fig.53.

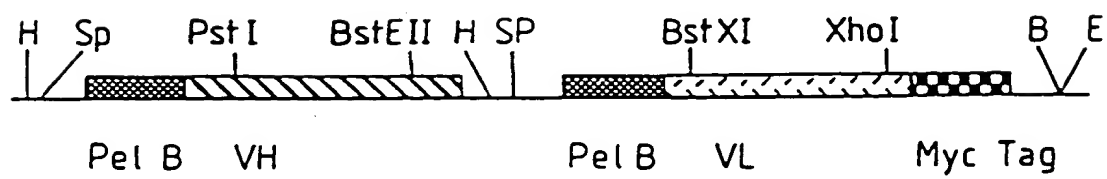


Fig.52.

	CDR 1	CDR 2
D1.3	DIQMTQSPASLSASVGETVTITCRASGNIHNYLA	WYQQKQKSPQLLVYYTTTLAD
M1F	DIELTQSPSSLSASLGERVSLTCRASQDIGSSLN	WLQQEPDGTIKRLIYATSSLDS
M21	DIELTQSPALMAASPGEKVTITCSVSSSISSSNLHWYQQKSETSPKPWIYGTSNLAS	

	CDR 3	
D1.3	GVPSRFGSGSGTQYSLKINSLQPEDFGSYQCQHFWSPTPTFGGGTKLEIKR	(SEQ ID NO. 266)
M1F	GVPKRFSGSRGSDYSLTISSLESEDFVDYYCLQYASPWTFGGGTKLELKR	(SEQ ID NO. 267)
M21	GVPVRFSGSGGTSYSLTISSMEAEDAATYYCQQWSSYPITFGAGTKLEIKR	(SEQ ID NO. 268)